

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 17, 2003, 11:33:06 ; Search time 83 seconds
Sequence: 1 RPNTSRRLPKGVKHLKDFPILPGEI 25
Title: SEQID2-NAT3
Perfect score: 136
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:
1: /SIDSL/gcldata/geneseq/geneseq/geneseqp-emb1/AA1980.DAT; *
2: /SIDSL/gcldata/geneseq/geneseq/geneseqp-emb1/AA1981.DAT; *
3: /SIDSL/gcldata/geneseq/geneseq/geneseqp-emb1/AA1982.DAT; *
4: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1983.DAT; *
5: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1984.DAT; *
6: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1985.DAT; *
7: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1986.DAT; *
8: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1987.DAT; *
9: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1988.DAT; *
10: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1989.DAT; *
11: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1990.DAT; *
12: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1991.DAT; *
13: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1992.DAT; *
14: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1993.DAT; *
15: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1994.DAT; *
16: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1995.DAT; *
17: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1996.DAT; *
18: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1997.DAT; *
19: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1998.DAT; *
20: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1999.DAT; *
21: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA2000.DAT; *
22: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA2001.DAT; *
23: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA2002.DAT; *
24: /SIDSL/gcldata/geneseq/geneseqp-emb1/AA2003.DAT; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	127	93.4	56	23 ABJ04946	A2 domain of fVII
2	127	93.4	294	23 AAC79422	Human factor VIII
3	127	93.4	368	16 AAR73020	Human Factor-VIII
4	127	93.4	720	16 AAR74088	Factor-VIII heavy
5	127	93.4	729	16 AAR74089	Factor-VIII heavy
6	127	93.4	740	16 AAR76961	Human Factor-VIII
7	127	93.4	740	16 AAR76962	Human Factor-VIII
8	127	93.4	740	16 AAR73021	Human Factor-VIII heavy
9	127	93.4	740	16 AAR74090	Factor-VIII heavy

ALIGNMENTS

RESULT 1	ABJ04946	standard; Protein; 56 AA.
ID	ABJ04946	
AC	ABJ04946	
XX		30-OCT-2002 (first entry)
DT		
XX		A2 domain of fVII epitope SEQ ID No 2.
DE		
XX		Haemostatic; antibody inhibitor; factor VIII; T cell; immune response; haemophilia A; acquired haemophilia; human factor VIII.
KW		
KW		
XX		Homo sapiens.
OS		
XX		WO200260917-A2.
PN		
XX		30-Nov-2001; 2001WO-US44945.
PD		
XX		08-AUG-2002.
PF		
XX		01-DEC-2000; 2000US-250430P.
PR		
XX		(MINU) UNIV MINNESOTA.
PA		
XX		Conti-fine BM;
PI		
XX		DR
WPI		2002-627462/67.
PT		New peptides or their variants, useful for preventing, treating or inhibiting aberrant or pathogenic production of antibodies specific for factor VIII, particularly useful for treating hemophilia A or acquired
PT		PT

PT hemophilia -
 XX Claim 2; Page 84; 120pp; English.
 PS The invention relates to isolated and purified peptides and variants
 XX thereof, as well as DNA encoding those peptides, useful to prevent or
 treat antibody inhibitors of factor VIII. The peptides are useful for
 preventing or inhibiting aberrant, pathogenic or undesirable antibody
 production or antibody binding that is specific for factor VIII. The
 peptides are also useful for preventing or inhibiting the priming or
 activity of T cells specific for factor VIII. These peptides are also
 useful for enhancing the activity or increasing the levels of modulatory
 T cells that inhibit the immune response to factor VIII. These peptides
 are useful in mammals, particularly in humans. The administration of
 these peptides does not increase the synthesis of a pathogenic antibody
 to factor VIII, or its biologically active fragment or functional
 equivalent. In particular, these peptides are useful for treating
 haemophilia A or acquired haemophilia. This sequence represents a human
 factor VIII protein region relating to the invention.

XX Sequence 56 AA;

Query Match 93.4%; Score 127; DB 23; Length 56;
 Best Local Similarity 96.0%; Pred. No. 3.3e-11;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPNTSRRRLPKGVKHLKDFPILPGEI 25
 5 RPLYSRRRLPKGVKHLKDFPILPGEI 29
 Db

RESULT 2

AAG79422
 ID AAG79422 standard; protein; 294 AA.
 XX AAG79422;

AC AC79422;
 XX DT 25-OCT-2002 (first entry)

XX DE Human factor VIII region 2/3.
 XX KW Factor VIII; factor IX; coagulation; blood; cardiovascular disorder;
 KW thrombosis; atherosclerosis; restenosis.
 XX PR 23-JAN-2001; 2001US-263431P.
 OS Homo sapiens.

XX PN WO200259268-A2.
 XX PD 01-AUG-2002.
 XX PF 23-JAN-2002; 2002WO-US01724.

XX DR 2002-599771/64.
 PA (UYSL-) UNIV SAINT LOUIS.
 XX PI Bajaj PS; Fay PJ;
 XX WPI; 2002-599771/64.

PT New polypeptide inhibits interaction of blood coagulation factor VIIIa
 PT with factor IXa precluding activation of factor X, useful for
 PT preventing or treating coagulation disorders, such as thrombosis,
 PT atherosclerosis and restenosis -

XX PS Claim 2; Fig 7A; 61PP; English.

XX The sequences given in AAG79422-23 represent regions 2 and 3 of human
 CC factors VIII and IX. Region 2 comprises the interaction between N346
 CC of factor IXa and E455 and K570 of factor VIIa, and the interaction
 CC between R403 of factor IXa and E633 of factor VIIa. Region 3 comprises
 the interaction between K293 of factor IXa and D712 of factor VIIIa, and
 CC the interaction between E410 of factor IXa and K713 of factor VIIa.

CC Fragments of these polypeptides inhibit the interaction of blood
 CC coagulation factor VIIIa with blood coagulation factor IXa. They also
 CC inhibit the activation of blood coagulation factor X, or inhibit blood
 CC coagulation. These peptide fragments are useful in preventing and/or
 CC treating coagulation disorders, in particular cardiovascular disorders
 CC such as thrombosis, atherosclerosis and restenosis.

XX Sequence 294 AA;

Query Match 93.4%; Score 127; DB 23; Length 294;
 Best Local Similarity 96.0%; Pred. No. 1.9e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPNTSRRRLPKGVKHLKDFPILPGEI 25
 5 RPLYSRRRLPKGVKHLKDFPILPGEI 29

Db

RESULT 3

AAR73020 standard; peptide; 368 AA.

XX ID AAR73020
 XX AC AAR73020;
 XX DT 25-MAR-2003 (updated)
 XX DR 21-NOV-1995 (first entry)

XX DE Human Factor-VIII fragment.
 XX KW Factor-VIII; blood-clotting; blood; coagulant; haemophilia A.
 XX OS Homo sapiens.

XX PN WO9513301-A1.
 XX PD 18-MAY-1995.
 XX PP 10-NOV-1994; 94WO-DK00424 .
 XX PR 12-NOV-1993; 93DK-0001281 .
 XX PA (NOVO) NOVO-NORDISK AS .
 XX PI Person E;

XX DR WPI; 1995-194038/25.
 XX PT Crosslinked Factor VIII polypeptide which is stable - is prep'd. using
 PT bis(sulphosuccinimidyl) suberate or disuccinimidyl suberate in the
 PT presence of polysorbate 80 to produce a coagulant with long lasting
 PT activity

XX XX Disclosure; Page 19; 36pp; English.

XX XX This is a fragment corresponding to internal AAs 373-740 of human
 CC Factor-VIII which may be crosslinked resulting in
 CC increased stability and retention of high activity over extended
 CC periods of time after activation by thrombin. The polypeptide is
 CC used to prevent or treat diseases caused by the absence or deficiency
 CC of Factor-VIII in a subject such as haemophilia.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 368 AA;

Query Match 93.4%; Score 127; DB 16; Length 368;

Best Local Similarity 96.0%; Pred. No. 2.4e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPNTSRRRLPKGVKHLKDFPILPGEI 25
 5 RPLYSRRRLPKGVKHLKDFPILPGEI 136

Db

RESULT 4
 AAR74088
 ID AAR74088 standard; protein: 720 AA.
 XX AC AAR74088;
 XX DT 25-MAR-2003 (updated)
 DT 04-NOV-1995 (first entry)
 DE Factor-VIII heavy chain N-terminal fragment.
 XX KW human; Factor VIII; heavy chain; N-terminal fragment;
 XX thrombin cleavage; blood-clotting.
 OS Homo sapiens.
 PN WO9513300-A1.
 PD 18-MAY-1995.
 PF 10-NOV-1994; 94WO-DK00423.
 PR 12-NOV-1993; 93DK-0001280.
 PA (NOVO) NOVO-NORDISK AS.
 PI Ezban Rasmussen M, Kjalleke M;
 WPI: 1995-194037/25.
 DR XX
 PT Factor VIII polypeptide(s) comprising a heavy chain shorter than native Al-A2 domain - are easier to produce recombinantly and retain coagulant activity, may be used to treat patients who have developed antibodies to C-terminal epitope(s) of Factor VIII
 PT XX
 PS Claim 2; Page 27-29; 51pp; English.
 XX
 XX The sequence represents N-terminal residues 1-729 of a human Factor-VIII heavy chain. The sequence is shorter than the Al-A2 domain, and is produced by treating a polypeptide containing the full Al-A2 domain of full-length Factor-VIII with a protease, e.g. thrombin. The fragment has the same coagulant specific activity as full-length Factor-VIII in a chromogenic assay, and is activated by thrombin at a similar rate. The fragment may be produced recombinantly to reduce production costs and improve safety, and production levels and stability are higher than for the full-length form. The fragment may be used to treat patients who have developed antibodies against epitopes in the C-terminal part of the heavy chain.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 SQ Sequence 729 AA;
 Query Match 93.4%; Score 127; DB 16; Length 729;
 Best Local Similarity 96.0%; Pred. No. 5.e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0:
 QY 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRRLPKGVVKHLKDFPILPGEI 508
 XX
RESULT 5
 AAR74089
 ID AAR74089 standard; protein: 729 AA.
 XX AC AAR74089;
 XX DT 25-MAR-2003 (updated)
 DT 04-NOV-1995 (first entry)
 XX DE Factor-VIII heavy chain N-terminal fragment.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 692 /label= absent or Ala, Thr, Ser, Gly or Asp
 FT Misc-difference 720 /label= absent or Gln, Ser, Thr, Val or Ala
 FT Misc-difference 729 /label= absent or Val, Ala or Ile
 XX

PN WO9518827-A1.
 XX PI Ezban Rasmussen M, Nicolaisen EM, Persson E;
 PD XX DR WPI; 1995-255039/33.

XX Novel factor VIII derivative used to treat haemophilia - and
 PT comprises a functional A2 domain containing a mutation at one or
 PT more Cys residues.
 XX Disclosure; Page 18-20; 30pp; English.

PS XX The new Factor-VIII derivative comprises a functional A2 domain in
 CC which Cys-692 is replaced with Ser. For other (less preferred)
 CC substitutions at this site, see AAR76961. Alternatively, Glu-720 and/or
 CC Tyr-729 are deleted or substituted with various amino acids (as in
 CC the Features). The new derivative has the same activity as the wild-
 type Factor-VIII but with improved stability (the activity is
 CC maintained for a longer period compared to the rapid decline of the
 CC activity of wt Factor-VIII). The new derivative can be used in a
 CC composition for treating diseases caused by an absence or deficiency
 CC of Factor-VIII, especially haemophilia.

XX SQ Sequence 740 AA;

Query Match 93.4%; Score 127; DB 16; Length 740;
 Best Local Similarity 96.0%; Pred. No. 5.2e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPNTSRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 8
 AAR73021
 ID AAR73021 standard; Peptide: 740 AA.
 XX AC AAR73021;
 XX DT 25-MAR-2003 (updated)
 DT 21-NOV-1995 (first entry)
 DE Human Factor-VIII N-terminal fragment.
 XX KW Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A.
 XX OS Homo sapiens.
 XX PN WO9513301-A1.
 XX PR 12-NOV-1993; 93DK-0001281.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX Person E;
 XX PI WPI; 1995-194038/25.

RESULT 7
 AAR76962
 ID AAR76962 standard; protein; 740 AA.
 XX AC AAR76962;
 XX DT 09-MAR-1996 (first entry)
 DE Human Factor-VIII derivative.
 XX KW Factor-VIII; therapeutic; blood-clotting.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 692
 FT /label= Cys substituted by ser
 FT Misc-difference 720
 FT /label= absent or Gln, Ser, Thr, Val or Ala
 FT Misc-difference 729
 FT /label= absent or Val, Ala or Ile
 XX PN WO9518827-A1.
 XX PD 13-JUL-1995.
 XX PF 06-JAN-1995; 95WO-DK00008.
 XX PR 07-JAN-1994; 94DK-0000032.
 XX PA (NOVO) NOVO-NORDISK AS.

PS XX This is the N-terminal fragment of human Factor-VIII which may be
 CC crosslinked resulting in increased stability and retention of high
 CC activity over extended periods of time after activation by thrombin.
 CC The polypeptide is used to prevent or treat diseases caused by the

CC absence or deficiency of Factor VIII in a subject such as
 CC haemophilia.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 740 AA;

Query Match	93.4%	Score 127;	DB 16;	Length 740;
Best Local Similarity	96.0%	Pred. No. 5.2e-10;		
Matches 24; Conservative	0;	Mismatches 1;	Indels 0;	Gaps C;

QY i RPNYSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 9 AAR74090

ID AAR74090 Standard; protein; 740 AA.

XX AAR74090;

AC AAR74090;

XX DT 25-MAR-2003 (updated)
 DT 04-NOV-1995 (first entry)

DE Factor-VIII heavy chain N-terminal fragment.

XX KW human; Factor VIII; heavy chain; N-terminal fragment;
 KW thrombin cleavage; blood-clotting.

XX OS Homo sapiens.

XX PN WO9513300-A1.

XX PD 18-MAY-1995.

XX PF 10-NOV-1994; 94WO-DK00423.

XX PR 12-NOV-1993; 93DK-0001280.

XX PA (NOVO) NOVO-NORDISK AS.

PI Ezzban Rasmussen M, Kjalle M;

XX PS Disclosure; Page 30-32; 51pp; English.

XX DR WPI: 1995-194037/25.

PT The sequence represents N-terminal residues 1-740 of a human Factor-VIII heavy chain. The sequence contains entire A1 and A2 domains, and truncated forms (1-720 in (AAR74088) and 1-729 in (AAR74090)) may be produced by treatment with a protease, e.g. thrombin. The C-terminally truncated fragments have the same coagulant specific activity as full-length Factor-VIII, and may be produced recombinantly to reduce production costs and improve safety, giving higher production levels and stability than for the full-length form. The fragments may be used to treat patients who have developed antibodies against epitopes in the C-terminal part of the heavy chain. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 740 AA;

Query Match	93.4%	Score 127;	DB 16;	Length 740;
Best Local Similarity	96.0%	Pred. No. 5.2e-10;		
Matches 24; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 1 RPNYSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

Query Match 93.4%; Score 127; DB 16; Length 740;
 Best Local Similarity 96.0%; Pred. No. 5.2e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPNYSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

PT administered to haemophiliacs, i.e. factor VIII replacement therapy
XX XX PS D AAW33227 standard; protein: 1383 AA.
XX AC AAW33227 :
XX FT 30-APR-1998 (first entry)
XX DE Procoagulant-active human factor VIII; FVIII; haemophilia A;
XX KW recombinant secretion; pro-coagulant activity; resistance;
XX activated protein C cleavage; APC; B domain; A2 domain;
XX von Willebrand factor binding site; binding affinity;
XX FVIII replacement therapy.
XX DS Synthetic.
XX DS Homo sapiens.
XX Key Location/Qualifiers
XX Region 1..346 /note= "factor VIIIIA heavy chain"
XX Region 741..1383 /note= "factor VIIIIA light chain"
XX Domain 1..329 /note= "A1 domain"
XX Domain 1..179 /note= "plastocyanin-like domain 1"
XX Domain 187..329 /note= "plastocyanin-like domain 2"
XX Domain 380..711 /note= "A2 domain"
XX Misc_feature 711..746 /note= "a spacer of the sequence
XX SFSQNSRHPSTRQKQFNATTIPENDIEKTDPWF
XX AHRTDPMKIQNVSSSDLLML is inserted
XX between domains A2 and A3"
XX Domain 380..554 /note= "plastocyanin-like domain 3"
XX Domain 564..711 /note= "plastocyanin-like domain 4"
XX Domain 746..1073 /note= "A3 domain"
XX Domain 1073..1221 /note= "C1 domain"
XX Domain 1226..1378 /note= "C2 domain"
XX Cleavage-site 372..373 /note= "by thrombin"
XX Disulfide-bond 153..179 /note= "probable"
XX Disulfide-bond 528..554 /note= "probable"
XX Misc-difference 740 /label= R740A
XX /note= "wild type Arg replaced with Ala"
XX Key Location/Qualifiers
XX Region 1..346 /note= "factor VIIIIA heavy chain"
XX Region 741..1383 /note= "factor VIIIIA light chain"
XX Domain 1..329 /note= "A1 domain"
XX Domain 1..179 /note= "plastocyanin-like domain 1"
XX Domain 187..329 /note= "plastocyanin-like domain 2"
XX Domain 380..711 /note= "A2 domain"
XX MISC_feature 711..746 /note= "a spacer of the sequence
XX SFSQNSRHPSTRQKQFNATTIPENDIEKTDPWF
XX AHRTDPMKIQNVSSSDLLML is inserted
XX DR Amano K, Kaufman RJ, Pipe SW;
XX WPI; 1997-535830/49.
XX PT Modified human pro-coagulant active factor VIII - can be

between domains A2 and A3"

380..554 /note= "plastocyanin-like domain 3"
 564..711 /note= "plastocyanin-like domain 4"
 746..1073 /note= "A3 domain"
 1073..1221 /note= "C1 domain"
 1226..1378 /note= "C2 domain"

Cleavage-site 372..373 /note= "by thrombin"
 Disulfide-bond 153..179 /note= "probable"
 Disulfide-bond 528..554 /note= "probable"

Misc-difference 336 /label= R336I
 /note= "wild type Arg replaced with Ile"
 Misc-difference 562 /label= R562K
 /note= "wild type Arg replaced with Lys"
 Misc-difference 740 /label= R74CA
 /note= "wild type Arg replaced with Ala"

WO9740145-A1 .
 30-OCT-1997 .
 24-APR-1997; 97WO-US06563.
 15-MAY-1996; 96US-0017785.
 24-APR-1996; 96US-0016117.
 (UNMI) UNIV MICHIGAN.

Amano K, Kaufman RJ, Pipe SW;
 WPI; 1997-535830/49.

Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy

Claim 18; Page - ; 57pp; English.

The present sequence represents a novel pro-coagulant active factor VIII (FVIII) mutant protein, comprising a deletion of the B domain and von Willebrand factor binding site, mutations R336I, R562K and R74CA and an addition of an amino acid sequence spacer between the A2 and A3 domains. Factor VIII, along with calcium and phospholipid, acts as a cofactor for factor IXA, when it converts factor X to the activated form (factor XA). FVIII is the coagulation factor deficient in the X-chromosome-linked bleeding disorder haemophilia A. Several other mutant FVIII proteins have also been created (see AAW33222-29). The FVIII mutant F309S (AAW33225) is capable of recombinant secretion at higher levels than typically obtained with wild type FVIII and retains pro-coagulant activity. The FVIII mutant R336I (AAW33222) and R562K (AAW33223) are resistant to activated protein C (APC) cleavage. The FVIII mutant comprising a deletion of the B domain and von Willebrand factor binding site, a mutation at Arg740 and an addition of an amino acid sequence spacer between the A2 and A3 domains can form a more stable configuration, and have an approximate 5-fold increase in specific activity compared to purified wild type FVIII, while increasing their binding affinity to von Willebrand factor improves their stability. The FVIII proteins can be administered to haemophiliacs, i.e. FVIII replacement therapy, while the nucleic acid molecule can be used for gene therapy.

note: this sequence does not appear in the specification; it was created using sequences from the given references.

Query Match 93.4%; Score 127; DB 18; Length 1383;
 Best Local Similarity 96.0%; Pred. No. 1e-09;
 Matches 24; Conservative 0; Mismatches 1; Index 0; Gaps 0;

Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 13
 AAW33229
 ID AAW33229 standard; protein; 1383 AA.
 XX
 AC AAW33229;
 XX DT 30-APR-1998 (first entry)
 XX DE Procoagulant-active human factor VIII:C (FVIII) mutant protein.
 XX KW Pro-coagulant active factor VIII; FVIII; haemophilia A;
 KW recombinant secretion; pro-coagulant activity; resistance;
 KW activated protein C cleavage; APC; B domain; A2 domain; A3 domain;
 KW von Willebrand factor binding site; binding affinity;
 KW FVIII replacement therapy.
 XX OS Synthetic.
 OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 1..346 /note= "factor VIIIa heavy chain"
 FT Region 741..1383 /note= "factor VIIIa light chain"
 FT Domain 1..329 /note= "A1' domain"
 FT Domain 1..179 /note= "plastocyanin-like domain 1"
 FT Domain 187..329 /note= "plastocyanin-like domain 2"
 FT Domain 380..711 /note= "A2 domain"
 FT Misc_feature 711..746 /note= "a spacer of the sequence SFSQNNSRHPSTRKQFNATIPENDIEKTDPWF AHRTPMKPIQNVSSDLMLL is inserted between domains A2 and A3"
 FT Domain 380..554 /note= "plastocyanin-like domain 3"
 FT Domain 564..711 /note= "plastocyanin-like domain 4"
 FT Domain 746..1073 /note= "A3 domain"
 FT Domain 1073..1221 /note= "C1 domain"
 FT Domain 1226..1378 /note= "C2 domain"
 FT Cleavage-site 372..373 /note= "by thrombin"
 FT Disulfide-bond 153..179 /note= "probable"
 FT Disulfide-bond 528..554 /note= "probable"
 FT Misc-difference 309 /label= F309S /note= "wild type Phe replaced with Ser"
 FT Misc-difference 740 /label= R740A /note= "wild type Arg replaced with Ala"
 XX PN WO9740145-A1.
 XX PD 30-OCT-1997.

XX PF 24-APR-1997; 97WO-US06563.
 XX PR 15-MAY-1996; 96US-0017785.
 XX PR 24-APR-1996; 96US-0016117.
 XX PA (JNMI) UNIV MICHIGAN.
 PI Arano K, Kaufman RJ, Pipe SW;
 DR WPI; 1997-535830/49.

XX P: Modified human pro-coagulant active factor VIII - can be administered to haemophiliacs, i.e. factor VIII replacement therapy
 PS Claim 19; Page 7; 57pp; English.

XX The present sequence represents a novel pro-coagulant active factor VIII (FVIII) mutant protein, comprising a deletion of the B domain and von Willebrand factor binding site, mutations F309S, R740A and addition of an amino acid sequence spacer between the A2 and A3 domains. Factor VIII, along with calcium and phospholipid, acts as a cofactor for factor IXA, when it converts factor X to the activated form (factor XA). FVIII is the coagulation factor deficient in the X-chromosome-linked bleeding disorder haemophilia A. Several other mutant FVIII proteins have also been created (see AAW33222-29). The FVIII mutant F309S (AAW33225) is capable of recombinant secretion at higher levels than typically obtained with wild type FVIII and retains pro-coagulant activity. The FVIII mutant R336I (AAW33222) and R562K (AAW33223) are resistant to activated protein C (APC) cleavage. The present FVIII mutant can form a more stable configuration, and have an approximate 5-fold increase in specific activity compared to purified wild type FVIII, while increasing their binding affinity to von Willebrand factor improves their stability. The FVIII proteins can be administered to haemophiliacs, i.e. FVIII replacement therapy, while the nucleic acid molecule can be used for gene therapy. note: this sequence does not appear in the specification; it was created using sequences from the given references.

XX SQ Sequence 1383 AA;

Query Match 93.4%; Score 127; DB 9; Length 1383;
 Best Local Similarity 96.0%; Pred. No. 1e-09;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 DB 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 14
 AAP80268 ID AAP80268 standard; protein; 1424 AA.
 XX AC AAP80268;
 XX DR 25-MAR-2003 (updated)
 XX DT 10-OCT-1990 (first entry)
 DE Modified factor VIII:C sequence with the R740-D1658 deletion.
 XX KW Modified factor VIII:C; maturation polypeptide; haemophilia;
 KW blood coagulation; RD deletion; procoagulant.
 XX OS Homo sapiens.
 XX PN WO8800831-A.
 XX PD 11-FEB-1988.
 XX PF 31-JUL-1987; 87WO-US01814.
 PR 01-AUG-1986; 86US-0893375.

XX PA (BIOJ) BIOGEN NV.
 PA (PASE/) PASEK M P.
 XX PT Pasek MP;
 XX DR WPI; 1988-049866/07.
 DR N-PSDB; AAN80447.

XX PT New DNA sequences encoding modified factor VIII:C - with deletion of DNA encoding maturation polypeptide, useful for high yield transformation.
 XX PS Claim 3; Page 60-61-62-63; 97pp; English.

XX The RD deletion removes the DNA from Ser 741 to Ser 1657.
 CC A major part of the sequence encoding the maturation polypeptide of factor VIII:C is deleted, i.e. Gln 744 - ASP 1563.
 CC The full lenght Factor VIII:C cDNA has two changes with respect to the published sequence (EPO application 160457):
 CC CTG to CTA at Leu 242 and TTC to CRC change at amino acid residue 1880 (Phe t> Leu). The product is produced in approx. 20 times higher yields than previous recombinant produced factor VIII:C and are more easily purified. The peptide is used for treating haemophilia A, both acute and prolonged bleeding.
 CC See also AAN80444 and AAN80446.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 1424 AA;
 Query Match 93.4%; Score 127; DB 9; Length 1424;
 Best Local Similarity 96.0%; Pred. No. 1e-09;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 DB 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 15
 AAP91169 ID AAP91169 standard; protein; 1424 AA.
 XX AC AAP91169;
 XX DT 25-MAR-2003 (updated)
 DT 26-JUN-1990 (first entry)
 DE Sequence of 740 Arg-1649 Glu human Factor VIII:C.
 XX KW Human Factor VIII:C; Ad.RE.neo; 740 Arg-1649 Glu Factor VIII:C;
 KW haemophilia A.
 XX OS Homo sapiens.
 XX PN EP306968-A.
 XX PD 15-MAR-1989.
 XX PF 09-SEP-1988; 88EP-0114769.
 XX PR 10-SEP-1987; 87JP-0225147.
 PR 08-APR-1988; 88JP-0085454.
 XX PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.
 PA (TEIJ) TEIJIN LTD.
 XX PI Sugiyama T, Masuda K, Tajima Y, Yonemura H;
 XX DR WPI; 1989-078467/11.
 DR N-PSDB; AAN90654.
 XX PT Prodn. of recombinant human Factor-VIII-C - using animal cells transformed with a vector contg. the gene for

PT Factor VIII:C and a promoter
 XX Disclosure; Fig 1; 32pp; English.
 XX Arg-740 of the carboxyl terminus of the H chain is
 CC directly bonded by a peptide bond to Glu-1649 of the amino terminus of
 CC L chain. A prefd. expression vector used to transform animal cell so
 CC that they produce human Factor VIII:Cis plasmid Ad.RE.neo.
 CC The expression vector has at least one promoter upstream of AN90654.
 CC The transformants can constantly and continuously produce human Factor
 CC VIII:C in high yield on a commercial scale. The human Factor VIII:C so
 CC produced is considered to corresp. to the smallest species of active and
 CC intact Factor VIII:C molecules in the human blood plasma. It is useful
 CC for treating haemophilia A patients.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 1424 AA;

Query Match 93.4%; Score 127; DB 1C; Length 1424;
 Best Local Similarity 96.0%; Pred. No. 1e-09;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPNYSRRLPKGVKHLKDFFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFFPILPGEI 508

Search completed: October 17, 2003, 11:35:08
 Job time : 83 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	127	93.4	2351	1	EZHU		coagulation factor VIII precursor [validated] - human
2	94	69.1	2319	2	A47004		N; Alternate names: antihemophilic factor A; coagulation factor VIII; procoagulant C
3	75	55.1	2133	2	T42763		C; Species: Homo sapiens (man)
4	51	37.5	1607	2	T04583		C; Date: 28-Aug-1985 * sequence_revision 28-Aug-1985 # text_change 08-Dec-2000
5	50	36.8	958	2	A82583		C; Accession: 154318; A00525; T58059; A23584; A26174; A42348; A43986; S63527; S66445;
6	49	36.0	412	2	G71070		R; Gitschier, J.; Wood, W.I.
7	48.5	35.7	406	2	JC4591		Hum. Mol. Genet. 1, 199-200, 1992
8	48.5	35.7	405	2	B36340		A; Title: Sequence of the exon-containing regions of the human factor VIII gene.
9	48.5	35.7	433	2	A57596		A; Reference number: 154318; MUID:93265012; PMID:1303178
10	48.5	35.7	1253	2	T45787		A; Accession: 154318
11	48	35.3	156	2	B83164		A; Status: preliminary; translated from GB/EMBL/DDBJ
12	48	35.3	264	2	AC2515		A; Molecule type: DNA
13	48	35.3	600	2	B45642		A; Residues: 1-1921, 'S', 1923-2351 <RES>
14	48	35.3	1690	2	T40847		A; Cross-references: GB:N88648; NID:9182361; PIDN:AAA52420.1; PMID:9182383
15	47	34.6	444	2	S54011		R; Wood, W.I.; Capon, D.J.; Eaton, D.L.; Gitschier, J.; Keyt, B.; See
16	46	33.8	308	2	S67657		Nature 312, 330-337, 1984
17	46	33.8	348	2	G71681		A; Title: Expression of active human factor VIII from recombinant DNA clones.
18	46	33.8	467	2	T38353		A; Reference number: A00525; MUID:85061548; PMID:6436526
19	46	33.8	480	2	A99164		A; Accession: A00525
20	46	33.8	519	2	S77572		A; Residues: 1-2351 <WOO>
21	46	33.8	885	2	T38387		A; Cross-references: EMBL:X01165; EMBL:X01179
22	46	33.8	1001	2	C88779		R; Toole, J.J.; Knopf, J.L.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.
23	46	33.8	1023	2	A59431		S., D.N.; Hewick, R.M.
24	46	33.8	1038	2	T25033		Nature 312, 342-347, 1984
25	45.5	33.5	161	2	F75633		A; Title: Molecular cloning of a cDNA encoding human antihaemophilic factor.
26	45.5	33.5	246	2	H82553		A; Residues: 1-74, 'V', 76-1259, 'E', 1261-2351 <RE2>
27	45.5	33.5	554	2	B90679		A; Cross-references: GB:K01740; NID:9182802; PIDN:AAA52484.1; PMID:9182803
28	45.5	33.5	554	2	F85529		R; Truett, M.A.; Blacher, R.; Burke, R.L.; Caput, D.; Chu, C.; Dina, D.; Hartog, K.; B.; Randolph, A.; Urdea, M.S.; Valenzuela, P.; Dahl, H.H.; Favalaro, J.; Hansen, J.
29	45.5	33.5	554	2	C64762		DNA 4, 333-349, 1985

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query	Match	Length	DB	ID	Description
1	127	93.4	2351	1	EZHU		coagulation factor VIII precursor [validated] - human
2	94	69.1	2319	2	A47004		coagulation factor
3	75	55.1	2133	2	T42763		coagulation factor
4	51	37.5	1607	2	T04583		TMV resistance protein
5	50	36.8	958	2	A82583		conserved hypothetical protein
6	49	36.0	412	2	G71070		hypothetical protein
7	48.5	35.7	406	2	JC4591		alpha-1,3-fucosyltransferase
8	48.5	35.7	405	2	B36340		alpha(1,3)-fucosyltransferase
9	48.5	35.7	433	2	A57596		alpha-1,3-fucosyltransferase
10	48.5	35.7	1253	2	T45787		disease resistance
11	48	35.3	156	2	B83164		conserved hypothetical protein
12	48	35.3	264	2	AC2515		hypothetical protein
13	48	35.3	600	2	B45642		DNA-directed DNA polymerase
14	48	35.3	1690	2	T40847		probable rRNA binding protein
15	47	34.6	444	2	S54011		1-aminoacyclopropanol
16	46	33.8	308	2	S67657		hypothetical protein
17	46	33.8	348	2	G71681		hypothetical protein
18	46	33.8	467	2	T38353		serine hydroxymethyl
19	46	33.8	480	2	A99164		hypothetical protein
20	46	33.8	519	2	S77572		oligopeptide transporter
21	46	33.8	885	2	T38387		hypothetical protein
22	46	33.8	1001	2	C88779		protein T2D3.9 [in KIAA0013 protein]
23	46	33.8	1023	2	A59431		hypothetical protein
24	46	33.8	1038	2	T25033		hypothetical protein
25	45.5	33.5	161	2	F75633		3-demethylubiquinone
26	45.5	33.5	246	2	H82553		3-(3-hydroxyphenyl
27	45.5	33.5	554	2	B90679		3-(3-hydroxyphenyl
28	45.5	33.5	554	2	F85529		probable monooxygenase
29	45.5	33.5	554	2	C64762		

Biochemistry 31, 3315-3325, 1992
 A;Title: Identification and functional importance of tyrosine sulfate residues within re
 A;Reference number: A42348; MUID:92207952; PMID:1554716
 A;Molecule type: protein
 A;Accession: A42348
 A;Residues: 'X',517-523;1853-1860,'X','1862-1864,'X',1866 <FAY>
 R;Leyte, A.; van Schijndel, H.B.; Niehrs, C.; Huttner, W.B.; Verbeet, M.P.; Mertens, K.;
 J. Biol. Chem., 266, 740-746, 1991
 A;Title: Sulfation of Tyr(1680) of human blood coagulation factor VIII is essential for
 A;Reference number: A56109; MUID:91093266; PMID:1898735
 A;Contents: annotation; sulfation; suifatation; suifatation; suifatation; suifatation
 R;Gitschier, J.; Wood, W.I.; Goralka, T.M.; Wong, K.L.; Chen, E.Y.; Eaton, D.H.; Vehar,
 Nature 312, 326-330, 1984
 A;Title: Characterization of the human factor VIII gene.
 A;Reference number: A56196; MUID:6436525
 A;Contents: annotation; introns
 R;McMullen, B.A.; Fujikawa, K.; Davies, E.W.; Hedner, U.; Ezban, M.
 Protein Sci. 4, 740-746, 1995
 A;Title: Locations of disulfide bonds and free cysteines in the heavy and light chains of
 A;Reference number: A56216; MUID:95333127; PMID:7613471
 A;Contents: annotation; disulfide bonds
 A;Note: 329-Cys, 711-Cys, and 2019-Cys were shown to have free sulphydryls
 R;Kjalke, M.; Heding, A.; Talbo, G.; Persson, E.; Thomsen, J.; Ezban, M.
 Eur. J. Biochem. 234, 773-779, 1995
 A;Title: Amino acid residues 721-729 are required for full factor VIII activity.
 A;Reference number: S63527; MUID:96163459; PMID:8575434
 A;Accession: S63527
 A;Molecule type: protein
 A;Residues: 733-752;753-759 <KJA>
 R;Lind, P.; Larsson, K.; Spira, J.; Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg
 Eur. J. Biochem. 232, 19-27, 1995
 A;Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
 A;Reference number: S66445; MUID:96048024; PMID:7556150
 A;Accession: S66445
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1668-1685 <LIN>
 C;Comment: Factor VIII is activated by factor Xa and thrombin, but prolonged exposure to
 C;Genetics: A;Gene: GDB:F8C
 A;Cross-references: GDB:119124; OMIM:306700
 A;Map Position: Xq28-Xq28
 A;Introns: 48/2; 89/1; 130/1; 201/1; 224/1; 263/1; 337/1; 424/2; 481/3; 513/1; 584/3; 63
 C;Function:
 A;Description: acts as a cofactor, with calcium and phospholipid, for the factor Xa pro
 A;Pathway: blood coagulation
 C;Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxidase
 C;Keywords: acute phase; blood coagulation; duplication; glyccoprotein; hemophilia A; pig
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-2351/Product: coagulation factor VIII #status experimental <MAT>
 F;20-740/Product: coagulation factor VIII heavy chain #status experimental <ACH>
 F;20-356/Domain: A1 <DA1>
 F;23-348/Domain: ferroxidase repeat homology <FO1>
 F;402-730/Domain: ferroxidase repeat homology <FO2>
 F;760-1667/Domain: B <DB0>
 F;1668-2351/Product: coagulation factor VIII light chain #status experimental <AC1>
 F;1709-2038/Domain: A3 <DA3>
 F;1716-2038/Domain: ferroxidase repeat homology <FO3>
 F;2039-2191/Domain: C2 <DC1>
 F;2039-2188/Domain: discoidin I amino-terminal homology <DN1>
 F;2192-2351/Domain: C2 <DC2>
 F;2192-2345/Domain: discoidin I amino-terminal homology <DN2>
 F;60,258,601,76,803,847,919,962,982,1020,1024,1074,1274,1301,1319,1403,1

F;172-198,267-348,547-573,649-730,1851-1877,1918-1922,2040-2188/Disulfide bonds: #st
 F;355-356/Cleavage site: Arg-Met (coagulation factor Xa, protein C) *status predicted
 F;365,737,738,742,1683,1699/Binding site: sulfate (Tyr) (covalent) #status experimen
 F;391-392/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimen
 F;414,426/Binding site: sulfate (Tyr) (covalent) #status predicted
 F;759-760/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimen
 F;1667-1668/Cleavage site: Arg-Glu (unidentified proteinase) *status experimental
 F;1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimen
 F;1740-1741/Cleavage site: Arg-Ala (coagulation factor Xa) *status experimental
 F;2193-2345/Disulfide bonds: *status predicted
 Query Match Score 93.4%; Score 127; DB 1; Length 2351;
 Best Local Similarity 96.0%; Pred. No. 2.6e-10;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 ||| ||||| ||||| ||||| ||||| |||||
 Db 503 RPLYSRRLPKGVKHLKDFPILPGEI 527
 RESULT 2
 A47004
 coagulation factor VIII Precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Sep-1994 *sequence_revision: 09-Sep-1994 *text_change 18-Jun-1999
 C;Accession: A47004
 R;Elder, B.; Gitschier, J.
 Genomics 16, 374-379, 1993
 A;Title: Sequence of the murine factor VIII cDNA.
 A;Reference number: A47004; MUID:93300511; PMID:8314577
 A;Accession: A47004
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: GB:L05573; PID:AAA37385.1; PID:g192457
 C;Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxi
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;23-349/Domain: ferroxidase repeat homology <FO1>
 F;402-730/Domain: ferroxidase repeat homology <FO2>
 F;1686-2006/Domain: ferroxidase repeat homology <FO3>
 F;2007-2156/Domain: discoidin I amino-terminal homology <DN1>
 F;2150-2313/Domain: discoidin I amino-terminal homology <DN2>
 Query Match Score 69.1%; Score 94; DB 2; Length 2319;
 Best Local Similarity 66.7%; Pred. No. 2.2e-05;
 Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PNYSRRLPKGVKHLKDFPILPGEI 25
 ||| :|||:|||:|||:|||:|||
 Db 504 PLHARRRLPRGIKHVKDLPHPGEI 527
 RESULT 3
 T42763
 coagulation factor VIII precursor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 11-Jan-2000 *sequence_revision: 11-Jan-2000 *text_change 09-Jun-2000
 C;Accession: T42763
 R;Loilier, P.
 submitted to the EMBL Data Library, August 1996
 A;Reference number: Z22269
 A;Accession: T42763
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-2133 <LOL>
 A;Cross-references: EMBL:U49517; NID:91511633; PID:g1511634; PID:AA06705.1
 C;Superfamily: coagulation factor VIII; discoidin I amino-terminal homology; ferroxi
 C;Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia A;
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-2133/Product: coagulation factor VIII *status predicted <MAT>
 F;23-349/Domain: ferroxidase repeat homology <FO1>
 F;402-730/Domain: ferroxidase repeat homology <FO2>
 F;1498-1820/Domain: ferroxidase repeat homology <FOX3>

A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Tsubakai, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovskii-Almeida, S.; Vettore, A.L.
A; Reference number: A59328
A; Contents: annotation
C; Genetics:
A; Gene: XF2237

Query Match 55.1%; Score 75; DB 2; Length 2133;
Best Local Similarity 83.3%; Pred. No. 0.014;
Matches 15; Conservative 0; Mismatches 3; Indels 6; Gaps 0;

RESULT 4

QY 7 RLPKGVKHLKDFPILP 24
DB 509 RLLKGWKLKQMPILP 526

TMV resistance protein N homolog F23E13.30 - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 *text_change 17-Nov-2000
C;Accession: T04583; T05507
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
A;Reference number: T04583
A;Molecule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
R;Bevan, M.; Wedder, H.; Wambutt, R.; Hoheisel, J.; Newes, H.W.; Mayer, K.F.X.; Schucile submitted to the Protein Sequence Database, April 1998
A;Reference number: 215418
A;Accession: T05507
A;Molecule type: DNA
A;Residues: 1449-1607 <BE2>
A;Cross-references: EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetics:
A;Map position: 4
A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270

Query Match 37.5%; Score 51; DB 2; Length 2607;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 NYSRRLPKGVKHLKD 17
DB 973 HYSLRLPKGLKFPLD 987

RESULT 4

QY 6 RRLPKGVVKHLKDFPILP 22
DB 124 RRIPKGVIQETPDITIIP 140

Pyrococcus horikoshii hypothetical protein Ph1259 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Accession: G71070
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 *text_change 20-Jun-2000
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogi, DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic bacterium
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71070
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-412 <KA>
A;Cross-references: GB:AP000005; NID:932336132; PID:BAA30361.1; PMID:g3257678
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1259
C;Superfamily: hypothetical protein H10333

Query Match 36.0%; Score 49; DB 2; Length 412;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PNYSRRLPKGVKHLKDF 18
DB 146 PIFSERTPKYLKALKDF 156

RESULT 5

QY 7 JC4591 alpha-1,3 fucosyltransferase (EC 2.4.1.-) - mouse
C;Species: Mus musculus (house mouse)
C;Accession: JC4591
R;Ozawa, M.; Muramatsu, T.
J. Biochem. 119, 302-308, 1996
A;Title: Molecular cloning and expression of a mouse alpha-1,3 fucosyltransferase gene
A;Reference number: JC4591; MUID:97037075; PMID:8882722
A;Accession: JC4591
A;Molecule type: mRNA
A;Residues: 1-400 <OZA>
A;Cross-references: DDBJ:D63379

Query Match 35.7%; Score 48.5; DB 2; Length 400;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 RPNSRRRLPKGV-KHLKDFP 19

Xylella fastidiosa (strain 9a5c) conserved hypothetical protein XF2237 [imported] - *Xylella fastidiosa* (strain 9a5c)
C;Species: *Xylella fastidiosa*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 *text_change 20-Aug-2000
C;Accession: A82583
R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis, Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-958 <SIM>
A;Cross-references: GB:AE004036; GB:AE003849; NID:g9107384; PID:AAF85036.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Alves, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.; das-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laing, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Rodrigues, V.; Nunes, L.R.; Oliveira, M.R.; Oliveira, R.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa

Db 314 RANYERFVPRGAFIHVDDFP 333 A;Accession: A57596
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <GER>
C;Species: Homo sapiens (man)
C;Date: 20-Apr-2000 *sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: B36340; A36340; A41202
R;Goelz, S.E.; Hession, C.; Goff, D.; Griffiths, B.; Tizard, R.; Newman, B.; Chi-KOSSO, Cell 63, 1349-1356, 1990
A;Title: ELFT: a gene that directs the expression of an ELAM-1 ligand.
A;Reference number: A36340; MUID:91084863; PMID:1702034
A;Molecule type: mRNA
A;Accessories: GB:M58596; NID:9182068; PIDN:AAA63172.1; PID:9182069
A;Cross-references: A36340
A;Molecule type: mRNA
A;Residues: 'MRRLWGAARKPSGAGWEKEWAEAPQAWSGRLGPGR', 'SGRKGRAVPGWASWP AHLAAARPRLIGAGC'
A;Cross-references: GB:M58597; NID:9182070; PIDN:AAA63173.1; PID:9182071
A;Note: the codon used as an initiator for this translation is not in a good context for R;Low, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larsen, R.D.; Marks, E.M.; Macher, B.A. J. Biol. Chem. 266, 17467-17477, 1991
A;Title: Molecular cloning of a human fucosyltransferase gene that determines expression A;Reference number: A40976; MUID:91373370; PMID:1716630
A;Accession: A40976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86, 'P', 88-405 <LOW>
A;Cross-references: GB:M65030; NID:9182791; PIDN:AAA92977.1; PID:91236720
R;Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.
J. Biol. Chem. 266, 21777-21783, 1991
A;Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but does not encode ELFT-2.
A;Reference number: A41202; MUID:92042084; PMID:1716630
A;Accession: A41202
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240, 'D', 242-400 <KUM>
A;Cross-references: GB:S65161; NID:9239005; PIDN:AAB20349.1; PID:9239006
C;Genetics:
A;Gene: GDB:FUT4; CD15; FCT3A; FUC-TIV
A;Cross-references: GDB:131563; OMIM:104230
A;Map Position: 11q21-11q21
C;Superfamily: galactoside 3(4)-L-fucosyltransferase; hexosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-48/Domain: signal sequence #status predicted <SIG>
F;49-49/Product: alpha(1,3)-fucosyltransferase 4 #status predicted <MAT>
F;91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 35.78; Score 48.5; DB 2; Length 405;
Best Local Similarity 50.0%; Pred. No. 23; Mismatches 6; Indels 1; Gaps 1;
Matches 10; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
Qy 1 RPNSRRLPKGV-KHLKDFP 19
Db 319 RANYERFVPRGAFIHVDDFP 338 C;Accession: A57596
RESULT 9 A57596
A;Accession: A57596
A;Title: alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - :cuse
N;Alternate names: ELAM-1 ligand fucosyltransferase homolog
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 *sequence_revision 08-Feb-1996 #text_change 11-Jan-2000
C;Accession: A57596
R;Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak, B.; Kelly, R.J.; Hiraiwa, N.; Je J. Biol. Chem. 270, 25047-25056, 1995
A;Title: Molecular cloning, expression, chromosomal assignment, and tissue-specific expression.
A;Reference number: A57596; MUID:96027607; PMID:7559635
Query Match 35.38; Score 48; DB 2; Length 156;
Best Local Similarity 36.48%; Pred. No. 97; Mismatches 6; Indels 8; Gaps 0;
C;Genetics:
A;Gene: PA3847
A;Accession: B83164
A;Cross-references: GB:AE004802; GB:AE004091; NID:99950021; PIDN:AAG07234.1; GSPDB:GT
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 *sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83164
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; I.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:10984043
A;Accession: B83164
A;Cross-references: STO
A;Molecule type: DNA
A;Residues: 1-156 <STO>
Query Match 35.38; Score 48; DB 2; Length 156;
Best Local Similarity 36.48%; Pred. No. 97; Mismatches 6; Indels 8; Gaps 0;
C;Genetics:
A;Gene: PA3847
Qy 1 RPNSRRLPKGV-KHLKDFPILP 22

RESULT 12

AC2515 hypothetical protein alr7299 [imported] - Nostoc sp. (strain PCC 7120) plasmid PCC7120al

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AC2515

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchishi, Nakazaki, N.; Shimpoo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. AB1807; MUID:21595285; PMID:11759840

A;Accession: AC2515

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-264 <KUR>

A;Cross-references: GB:BA000020: PIDN:BAB78383.1; PID:917135837; GSPDB:GN00180

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: air7299

A;Genome: Plasmid

Query Match 35.3%; Score 48; DB 2; Length 264;

Best Local Similarity 58.8%; Pred. NO. 17; Mismatches 6; Indels 0; Gaps 0; C;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0; C;

Oy 8 LPKGVKHILKDFPILPGE 24

Db 232 ITAGLKHLSFDSLPLVPE 248

RESULT 13

B46642 DNA-directed DNA polymerase (EC 2.7.7.7) alpha/DNA primase (EC 2.7.7.-) complex 58K chain

C;Species: Mus musculus (house mouse)

C;Date: 21-Sep-1993 *sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C;Accession: B46642

R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Matsutani, M.; Uti, M.; Hanaka, F.

J. Biol. Chem. 268, 8111-8122, 1993

A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA polymerase α

A;Reference number: A46642; MUID:93216788; PMID:8463324

A;Accession: B46642

A;Status: Preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-600 <MIY>

A;Cross-references: GB:DI3546; NID:9303658; PIDN:BA002746.1; PID:q303659

A;Experimental source: FM3A cells

A;Note: sequence extracted from NCBI backbone (NCBIN:129148, NCBI_P:129149)

C;Keywords: nucleotidyltransferase

Query Match 35.3%; Score 48; DB 2; Length 600;

Best Local Similarity 26.1%; Pred. NO. 41; Mismatches 9; Indels 0; Gaps 0; C;

Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0; C;

Oy 3 NYSRRLPKGVKHILKDFPILPGEI 25

Db 279 SYGAQIPVDSLSELKEYSLFPGQV 30;

RESULT 14

T40847 probable rRNA biogenesis protein - fission yeast (*Schizosaccharomyces pombe*)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 *sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C;Accession: T40847

R;Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

Submitted to the EMBL Data Library, September 1998

A;Reference number: Z21951

A;Accession: T40847

Result No.	Score	Query	Match	Length	DB	ID	Description
1	127	93.4	2351	1	FA8_HUMAN	PG0451	homo sapien
2	94	69.1	2319	1	FA8_MOUSE	CG6194	mus musculus
3	75	55.1	2133	1	FA8_PIG	P12263	sus scrofa
4	54.5	40.1	239	1	UBIG_XANAC	Q8PKJ0	xanthomonas
5	54.5	40.1	239	1	UBIG_XANCP	Q8P8h2	xanthomonas
6	52	38.2	599	1	COE4_MOUSE	Q8k4j2	mus musculus
7	48.5	35.7	405	1	FUT4_HUMAN	P220B3	homo sapien
8	48.5	35.7	433	1	FUT4_MOUSE	Q11227	mus musculus
9	48	35.3	495	1	DPO2_RAT	Q89043	rattus norvegicus
10	48	35.3	600	1	DPO2_MOUSE	P33611	mus musculus
11	46	33.8	467	1	GLYD_SCHPO	Q13972	schizosaccharomyces pombe
12	45.5	33.5	246	1	UBIG_XYLFA	P77397	xylophaga fasicularis
13	45.5	33.5	554	1	MHPA_ECOLI	G55673	escherichia coli
14	45	33.1	438	1	MURA_SYNY3	Q91687	synchocystis sp. PCC6803
15	45	33.1	1032	1	ITA4_XENLA	P53420	xenopus laevis
16	45	33.1	1690	1	CA44_HUMAN	Q14031	homo sapien
17	45	33.1	1691	1	CA64_HUMAN	P41653	pinus taeda
18	45	33.1	2054	1	YCF2_PINTH	Q96y96	sulfolobus solfataricus
19	44.5	32.7	788	1	SYFB_THERMA	Q84307	thermotoxum phaseolus
20	44	32.4	130	1	RR11_MARPO	P053834	caenorhabditis elegans
21	44	32.4	300	1	ERA_MYCTU	P35800	mycobacterium ulcerans
22	44	32.4	356	1	CCDA_CAEEL	C27038	methanobacterium thermoautotrophicum
23	44	32.4	385	1	VATC_METTH	Q14993	homo sapien
24	44	32.4	1143	1	CAII_HUMAN	P17890	saccharomyces cerevisiae
25	43.5	32.0	251	1	RPCB YEAST	Q96y96	sulfolobus solfataricus
26	43.5	32.0	352	1	AROB_SULTO	Q84307	chlamydia trachomatis
27	43.5	32.0	649	1	VATI_CHLTR	Q96y96	phaseolus vulgaris
28	43	31.6	138	1	RR11_PHAAN	Q56425	aquifex aeolicus
29	43	31.6	146	1	YZ37_AQUAE	Q77302	lumbricus terrestris
30	43	31.6	156	1	RS10_LUMRU	Q07254	xenopus laevis
31	43	31.6	165	1	RS10_XENLA	Q90y94	ictalurus punctatus
32	43	31.6	166	1	RS10_ICTPU	Q57811	pyrococcus
33	43	31.6	227	1	FLPA_PYRHO		

RESULT 1							
FA8_HUMAN		STANDARD:		PRT; 2351 AA.			
ID	FA8_HUMAN	AC	P00451;	DT	21-JUL-1986 (Rel. 01, Created)	RA	Truett M.A., Blacher R.L., Caput D., Chu C., Dina J., Hartog K., Kuo C.H., Masiarz F.R., Merryweather J.P., Najarian R., Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A., Urdea M.S., Valenzuela P., Dahl H.-H.M., Favallaro J., Hansen J., Nordfang O., Ezban M.;
GN	Homo sapiens (Human)	FB OR FBC.		DE	Coagulation factor VIII precursor (Procoagulant component) (Antihemophilic factor) (AHF).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;			RN	"Characterization of the polypeptide composition of human factor VIII:C and the nucleotide sequence and expression of the human factor VIII:C and the nucleotide sequence and expression of the human kidney CDNA."	RT	
OC				RN	SEQUENCE FROM N.A. MEDLINE=86081164; PubMed=3935400;	RT	
OX				RX	"Characterization of the polypeptide composition of human factor VIII:C and the nucleotide sequence and expression of the human kidney CDNA."	RT	
				RA	Truett M.A., Blacher R.L., Caput D., Chu C., Dina J., Hartog K., Kuo C.H., Masiarz F.R., Merryweather J.P., Najarian R., Pachl C., Potter S.J., Puma J., Quiroga M., Rall L.B., Randolph A., Urdea M.S., Valenzuela P., Dahl H.-H.M., Favallaro J., Hansen J., Nordfang O., Ezban M.;	RA	
				RA	SEQUENCE FROM N.A. MEDLINE=85061548; PubMed=6438526;	RT	
				RA	Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J., Keyt B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L., Delwart E., Tuddenham E.G.D., Vehar G.A., Lawn R.M.; "Expression of active human factor VIII from recombinant DNA clones." Nature 312:330-337(1984).	RA	
				RA	SEQUENCE FROM N.A. MEDLINE=85061548; PubMed=6438526;	RT	
				RA	Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J., Keyt B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L., Delwart E., Tuddenham E.G.D., Vehar G.A., Lawn R.M.; "Expression of active human factor VIII from recombinant DNA clones." Nature 312:330-337(1984).	RA	
				RA	SEQUENCE FROM N.A. MEDLINE=85061550; PubMed=6438528;	RT	
				RA	Toole J.J., Knopf J.L., Wozney J.M., Sultzman L.A., Buecker J.L., Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C., Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Fass D.N., Howick R.M.; "Molecular cloning of a cDNA encoding human antihaemophilic factor." Nature 312:342-347(1984).	RA	
				RA	SEQUENCE FROM N.A. MEDLINE=85061550; PubMed=6438528;	RT	
				RA	Toole J.J., Knopf J.L., Wozney J.M., Sultzman L.A., Buecker J.L., Pittman D.D., Kaufman R.J., Brown E., Shoemaker C., Orr E.C., Amphlett G.W., Foster W.B., Coe M.L., Knutson G.J., Fass D.N., Howick R.M.; "Molecular cloning of a cDNA encoding human antihaemophilic factor." Nature 312:342-347(1984).	RA	
				RA	SEQUENCE FROM N.A. MEDLINE=93265012; PubMed=1303178;	RT	
				RA	Gitschier J., Wood W.I.; "Sequence of the exon-containing regions of the human factor VIII gene."	RT	
				RA	Hum. Mol. Genet. 1:199-200(1992).	RL	
				RA	SEQUENCE OF 2064-2070 FROM N.A.	RN	
				RA	de Water N.S., Williams R., Browett P.J.; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.	RL	
				RA	SULFATION OF TYR-1699.	RN	
				RP			

RX MEDLINE=91093266; PubMed=1898735;
 RA Leyte A., van Schijndel H.B., Niehrs C., Huttner W.B., Verbeet M.P.,
 RA Mertens K., van Mourik J.A.;
 RT "Sulfation of Tyr1680 of human blood coagulation factor VIII is
 essential for the interaction of factor VIII with von Willebrand
 factor";
 RT RL J. Biol. Chem. 266:740-746(1991).
 RN [7]

RP SULFATION RX MEDLINE=92207952; PubMed=1554716;
 RA Pittman D.D., Wang J.H., Kaufman R.J.;
 RT "Identification and functional importance of tyrosine sulfate
 residues within recombinant factor VIII";
 RL Biochemistry 31:3315-3325(1992).
 RN [8]

RP-- STRUCTURE BY NMR OF 2322-2343.
 RX MEDLINE=95200924; PubMed=7893714;
 RA Gilbert G.E., Baleja J.D.;
 RT "Membrane-binding peptide from the C2 domain of factor VIII forms an
 amphipathic structure as determined by NMR spectroscopy.";
 RL Biochemistry 34:3022-3031(1995).
 RN [9]

RN REVIEW ON MOLECULAR BASIS OF HEMA.
 RP MEDLINE=91221499; PubMed=1902642;
 RA Gitschier J.;
 RT "The molecular basis of hemophilia A.";
 RL And. N.Y. Acad. Sci. 614:89-96(1991).
 RN [10]

RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX MEDLINE=89088506; PubMed=2491949;
 RA White G.C. II, Shoemaker C.B.;
 RT "Factor VIII gene and hemophilia A.";
 RL Blood 73:1-12(1989).
 RN [11]

RP REVIEW ON MOLECULAR BASIS OF HEMA.
 RX Antonarakis S.E., Kazazian H.H., Tuddenham E.G.D.;
 RT "Molecular etiology of factor VIII deficiency in hemophilia A.";
 RL Hum. Mutat. 5:1-22(1995).
 RN [12]

RP VARIANT HEMA GLN-2326.
 RX Gitschier J., Wood W.I., Shuman M.A., Lawn R.M.;
 RT "Identification of a missense mutation in the factor VIII gene of a
 mild hemophiliac.";
 RL Science 232:1415-1416(1986).
 RN [13]

RP VARIANT HEMA PRO-2135.
 RX MEDLINE=88096539; PubMed=3122181;
 RA Levinson B., Janco R.L., Phillips J.A. III, Gitschier J.;
 RT "A novel missense mutation in the factor VIII gene identified by
 analysis of amplified hemophilia DNA sequences.";
 RL Nucleic Acids Res. 15:9797-9805(1987).
 RN [14]

RP VARIANT HEMA GLN-2228.
 RX MEDLINE=88191889; PubMed=2833855;
 RA Yousoufian H., Antonarakis S.E., Bell W., Griffin A.M.,
 RA Kazazian H.H.;
 RT "Nonsense and missense mutations in hemophilia A: estimate of the
 relative mutation rate at CG dinucleotides.";
 RL Am. J. Hum. Genet. 42:718-725(1988).
 RN [15]

RP VARIANT HEMA GLY-291.
 RX MEDLINE=88220354; PubMed=2835904;
 RA Yousoufian H., Wong C., Antonarakis S.E., Platokoukis H., Kazazian H.H.,
 RA Kazazian H.H.;
 RT "Moderate severe hemophilia A resulting from Glu-->Gly substitution
 in exon 7 of the factor VIII gene.";
 RL Am. J. Hum. Genet. 42:867-871(1988).
 RN [16]

RP VARIANT HEMA CYS-1708.
 RX MEDLINE=89274393; PubMed=2499363;
 RA O'Brien D.P., Tuddenham E.G.;

RT "Purification and characterization of factor VIII 1,689-Cys: a
 nonfunctional cofactor occurring in a patient with severe hemophilia
 A.";
 RT RL Blood 73:2117-2122(1989).
 RN [17]

RP VARIANT HEMA CYS-391.
 RX MEDLINE=90001543; PubMed=2506948;
 RA Shima M., Ware J., Yoshioka A., Fukui H., Fulcher C.A.;
 RT "An arginine to cysteine amino acid substitution at a critical
 thrombin cleavage site in a dysfunctional factor VIII molecule.";
 RL Blood 74:1612-1617(1989).
 RN [18]

RP VARIANT HEMA LEU-189.
 RX MEDLINE=9057680; PubMed=2510835;
 RA Chan V., Chan T.K., Tong T.M., Todd D.;
 RT "A novel missense mutation in exon 4 of the factor VIII:C gene
 resulting in moderately severe hemophilia A.";
 RL Blood 74:2688-2691(1989).
 RN [19]

RP VARIANT HEMA LEU-2326.
 RX MEDLINE=89197216; PubMed=2495245;
 RA Inaba H., Fujimaki M., Kazazian H.H. Jr., Antonarakis S.E.;
 RT "Mild hemophilia A resulting from Arg-to-Leu substitution in exon 26
 of the factor VIII gene.";
 RL Hum. Genet. 81:335-338(1989).
 RN [20]

RP VARIANT HEMA HIS-391.
 RX MEDLINE=89264602; PubMed=2498882;
 RA Arai M., Inaba H., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
 RA Fujimaki M., Hoyer L.W.;
 RT "Direct characterization of factor VIII in plasma: detection of a
 mutation altering a thrombin cleavage site
 (arginine-372->histidine).";
 RT PROC. Natl. Acad. Sci. U.S.A. 86:4277-4281(1989).
 RL [21]

RP VARIANT HEMA CYS-1708.
 RX MEDLINE=90105723; PubMed=2104766;
 RA Arai M., Higuchi M., Antonarakis S.E., Kazazian H.H. Jr.,
 RA Phillips J.A. III, Janco R.L., Boyer L.W.;
 RT "Characterization of a thrombin cleavage site mutation (Arg 1689 to
 Cys) in the factor VIII gene of two unrelated patients with
 cross-reacting material-positive hemophilia A.";
 RL Blood 75:384-389(1990).
 RN [22]

RP VARIANT HEMA GLN-2328 AND LEU-2326.
 RX MEDLINE=90123183; PubMed=2105106;
 RA Casula L., Murru S., Pecorara M., Ristaldi M.S., Restagno G.,
 RA Mancuso G., Morfini M., de Biasi R., Baudo F., Carbonara A.;
 RT "Recurrent mutations and three novel rearrangements in the factor
 VIII gene of hemophilia A patients of Italian descent.";
 RT Blood 75:662-670(1990).
 RL [23]

RP VARIANT HEMA CYS-391.
 RX MEDLINE=90329422; PubMed=1973901;
 RA Pattinson J.K., McVey J.H., Boon M., Ajani A., Tuddenham E.G.;
 RT "CRM+ haemophilia A due to a missense mutation (372-->Cys) at the
 internal heavy chain thrombin cleavage site.";
 RT Br. J. Haematol. 75:73-77(1990).
 RL [24]

RP VARIANT HEMA PHE-1699 AND CYS-1708.
 RX MEDLINE=90152691; PubMed=2105906;
 RA Higuchi M., Wong C., Kochhan L., Olek K., Aronis S., Kasper C.K.,
 RA Kazazian H.H., Antonarakis S.E.;
 RT "Characterization of mutations in the factor VIII gene by direct
 sequencing of amplified genomic DNA.";
 RL Genomics 6:65-71(1990).
 RN [25]

RP VARIANT HEMA CYS-1728 AND ASP-1941.
 RX MEDLINE=90169988; PubMed=2106480;
 RA Traystman M.D., Higuchi M., Kasper C.K., Antonarakis S.E.,
 RA Kazazian H.H.;
 RT "Use of denaturing gradient gel electrophoresis to detect point
 mutations in the factor VIII gene.";

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
 [2]
 RN SEQUENCE OF 705-1573 FROM N.A.
 RP MEDLINE-86:287369; PubMed-3016730;
 RX Toole J.J., Pittman D.D., Orr E.C., Murtha P., Wasiey L.C.,
 RA Kaufman R.J.;
 "A large region (approximately equal to 95 kDa) of human factor VIII
 is dispensable for *in vitro* procoagulant activity.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:5939-5942(1986).
 RL
 RN [3]
 RP SEQUENCE OF 392-759 FROM N.A.
 RX MEDLINE-94179260; PubMed-7510693;
 RA Lubin I.M., Healey J.F., Scandellari D., Runge M.S., Loijer P.;
 "Elimination of a major inhibitor epitope in factor VIII.";
 J. Biol. Chem. 269:8639-8641(1994).
 !- FUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSPHOLIPID, ACTS
 AS A COFACTOR FOR FACTOR IXA WHEN IT CONVERTS FACTOR X TO THE
 ACTIVATED FORM, FACTOR XA.
 !- SUBCELLULAR LOCATION: Extracellular.
 CC -! SIMILARITY: Contains 3 F5/8 type A domains.
 CC -! SIMILARITY: Contains 2 F5/8 type C domains.
 CC -! SIMILARITY: STRONG, TO COAGULATION FACTOR V.
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 DR EMBL; U49517; AABG6705; 1; -.
 DR PIR; A25945; A25945.
 DR PIR; T42763; T42763.
 DR HSSP; P00451; ICFG.
 DR InterPro; IPR0001117; Cu-oxidase.
 DR InterPro; IPR000421; FA58_C.
 DR Pfam; PF00394; Cu-oxidase; 3.
 DR SMART; SMO0231; FA58C; 2.
 DR PROSITE; PS01285; FA58C_1; 2.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS50022; FA58C_3; 2.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
 KW Blood coagulation; Repeat; Plasma; Acute phase; Caicum;
 Signal; Glycoprotein; Sulfation.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 2133 COAGULATION FACTOR VIII.
 FT DOMAIN 20 357 F5/8 TYPE A 1.
 FT DOMAIN 20 169 PLASTOCYANIN-LIKE 1.
 FT DOMAIN 207 357 PLASTOCYANIN-LIKE 2.
 FT DOMAIN 399 730 F5/8 TYPE A 2.
 FT DOMAIN 399 573 PLASTOCYANIN-LIKE 3.
 FT DOMAIN 583 730 F5/8 TYPE C 1.
 FT DOMAIN 760 1599 F5/8 TYPE C 2.
 FT DOMAIN 1495 1822 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT DOMAIN 1495 1659 PLASTOCYANIN-LIKE 5.
 FT DOMAIN 1669 1822 PLASTOCYANIN-LIKE 6.
 FT DOMAIN 1822 1970 F5/8 TYPE C 1.
 FT DOMAIN 1975 2127 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT SITE 391 392 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT SITE 759 760 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT SITE 1449 1450 CLEAVAGE (ACTIVATION) (BY SIMILARITY).
 FT MOD_RES 737 737 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 FT MOD_RES 738 738 SULFATION (BY SIMILARITY).
 FT MOD_RES 742 742 SULFATION (BY SIMILARITY).
 FT DISULFID 173 199 PROBABLE.
 FT DISULFID 547 573 PROBABLE.
 FT DISULFID 1633 1659 PROBABLE.
 FT DISULFID 1822 1970 BY SIMILARITY.
 FT DISULFID 1975 2127 BY SIMILARITY.
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 929 929 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 985 985 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1025 1025 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1111 1111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1181 1181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1208 1208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1245 1245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1265 1265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1335 1335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1408 1408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1611 1611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1919 1919 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 713 713 N->M (IN REF. 2).
 FT CONFLICT 734 734 I->T (IN REF. 2).
 FT CONFLICT 792 792 G->Q (IN REF. 2).
 FT CONFLICT 1133 1133 E->F (IN REF. 2).
 FT CONFLICT 1191 1191 I->L (IN REF. 2).
 FT CONFLICT 1209 1209 R->P (IN REF. 2).
 FT CONFLICT 1437 1437 C->G (IN REF. 2).
 FT CONFLICT 1456 1456 F->R (IN REF. 2).
 FT CONFLICT 1539 1539 F->R (IN REF. 2).
 FT CONFLICT 1546 1546 Q->N (IN REF. 2).
 SQ SEQUENCE 2133 AA; 239304 MW; 152BBA8997F570DA CRC64;
 Score 75; DB 1; Length 2133;
 Best Local Similarity 83.3%; Pred. No. 0.0052;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 RLPKGVKHLKDFFPILPGE 24
 5C9 RLLKGWKKHLKDMPLPGE 526

Db

RESULT 4
 UBIG_XANAC
 JD UBIG_XANAC STANDARD: PRT; 239 AA.
 AC Q8PK00;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-
 DE dihydroxy-5-hexapropylbenzoate methyltransferase) (DHBB
 DE methyltransferase).
 GN UBIG OR XAC2377.
 OS Xanthomonas axonopodis (Pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonas;
 OC Xanthomonadaceae; Xanthomonas.
 NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannarano F., Cardozo J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Gregorio C.C., Gruber A.,
 RA Katsuyama A.M., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Locali E.C., Machado M.A., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Martins E.C., Moreira L.M., Novo M.T.M., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos W., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.,
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 host specificities."
 RT Nature 417:459-463 (2002).
 RL -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-

CC

CC demethylubiquinone-9 + S-adenosyl-L-homocysteine + ubiquinone-9.
 CC -!- PATHWAY: Ubiquinone biosynthesis.
 CC -!- SIMILARITY: BELONGS TO THE UBIG/CCO3 FAMILY.

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DR EMBL; AE012334; AAM41548.1; -.
 DR HAMAP; MF_00472; -; -.
 DR InterPro; IPR001601; Methyltransfer.
 DR InterPro; IPR000051; SAM_bind.
 KW Ubiquinone biosynthesis; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 239 AA; 26060 MW; F56121516B27DFE6 CRC64;

Query Match 40.1%; Score 54.5%; DB 1; Length 239;
 Best Local Similarity 57.1%; Pred. No. 0.58;
 Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

RESULT 5
 ID UBIG_XANCP STANDARD; PRT: 239 AA.
 AC Q8PBH2;
 DT 28-FEB-2003 (Rel. 41. Last sequence update)
 DT 28-FEB-2003 (Rel. 41. Last annotation update)
 DE 3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB)
 DE methyltransferase.
 GN UBIG OR XCC2269.
 OS Xanthomonas campestris (Pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 Quaggio R.B., Monteiros-Vitorelo C.B., Van Sluys M.A., Aimeida K.F.,
 Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
 Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.N., Lemos M.V.F.,
 Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y.,
 Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 Pereira H.A., Rossi A., Sena J.A.D., Silva R.F., de Souza R.F.,
 Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 Trindade dos Santos M., Truffi D., Tsai S.M., White F.P.,
 Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."
 RL Nature 417:459-463 (2002).

-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
 -!- PATHWAY: Ubiquinone biosynthesis.
 -!- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.

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DR HAMAP; MF_00472; -; -.
 DR InterPro; IPR001601; Methyltransfer.
 DR InterPro; IPR000051; SAM_bind.
 KW Ubiquinone biosynthesis; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 239 AA; 26039 MW; 70BA381BAF14AC71 CRC64;

Query Match 40.1%; Score 54.5%; DB 1; Length 239;
 Best Local Similarity 57.1%; Pred. No. 0.58;
 Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 5 SRRLPKGVKHLKDFPILPGEI 25
 Db 177 ARLLPKGTHHYKDF-IKPSEL 196

RESULT 6
 COE4_MOUSE STANDARD; PRT: 599 AA.
 ID COE4_MOUSE ID Q8K4J1; Q8K4J3; Q8K4J5;
 AC Q8K4J2; Q8K4J1; Q8K4J3; Q8K4J5;
 DT 28-FEB-2003 (Rel. 41. Created)
 DT 28-FEB-2003 (Rel. 41. Last sequence update)
 DT 15-SEP-2003 (Rel. 42. Last annotation update)
 DE Transcription factor COE4 (Early B-cell factor 4) (Olf-1/EBF-like 4) (OE-4) (O/E-4).
 DE EBF4 OR COE4.
 CN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5), AND TISSUE SPECIFICITY.
 RP STRAIN=C57BL/6;
 RC MEDLINE=22136010; PubMed=12139918;
 RX Wang S.S., Betz A.G., Reed R.R.;
 RA "Cloning of a novel Olf-1/EBF-like gene, O/E-4, by degenerate oligo-based direct selection";
 RT Mol. Cell. Neurosci. 20:404-414 (2002).
 CC -!- FUNCTION: Seems to weakly activates transcription. Binds an Olf-1 consensus site in vitro.
 CC -!- SUBUNIT: Forms either a homodimer or a heterodimer with a related family member.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC -!- Event=Alternative splicing; Named isoforms=5;
 CC Name=3; Synonyms=4-23;
 CC IsoID=Q8K4J2-1; Sequence=Displayed;
 CC Name=1; Synonyms=4-11;
 CC IsoID=Q8K4J2-2; Sequence=VSP_001125, VSP_001126;
 CC Name=2; Synonyms=4-14;
 CC IsoID=Q8K4J2-3; Sequence=VSP_001121, VSP_001122;
 CC Name=4; Synonyms=4-132;
 CC IsoID=Q8K4J2-4; Sequence=VSP_001123, VSP_001124;
 CC Name=5; Synonyms=4S;
 CC IsoID=Q8K4J2-5; Sequence=VSP_001119, VSP_001120;
 CC -!- TISSUE SPECIFICITY: Expressed in the neuronal and basal cell layers of olfactory epithelium. Absent in the vomeronasal organ.
 CC -!- SIMILARITY: BELONGS TO THE COE FAMILY.

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Best Local Similarity 50.0%; Pred. No. 9.3;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 RPNSRRLPKGV-KHLKDFP 19
| : | : | : | : | : |
Db 347 RANYERFVPRGAFIHVDDEFP 366

SEQUENCE FROM N.A.
MEDLINE=96027607; PubMed=7559635;
RN SEQUENCE FROM N.A.
RX GERSTEN K.M., Natsuka S., Trinchera M., Petryniak B., Kelly R.J., Hiraiwa N., Jenkins N.A., Gilbert D.J., Copeland N.G., Lowe J.B.; RT "Molecular cloning, expression, chromosomal assignment, and tissue-specific expression of a murine alpha-(1,3)-fucosyltransferase locus corresponding to the human ELAM-1 ligand fucosyl transferase.";
RT J. Biol. Chem. 270:25047-25056(1995).
RN SEQUENCE FROM N.A. (ISOFORM SHORT).
RX STRAIN=129/SV; TISSUE=Liver;
RN MEDLINE=97037075; PubMed=8882722;
RA Ozawa M., Muramatsu T.;
RT "Molecular cloning and expression of a mouse alpha-1,3-fucosyltransferase gene that shows homology with the human alpha-1,3-fucosyltransferase IV gene.";
RT RIL Biochem. 119:302-308(1996).
CC -!- FUNCTION: May catalyze alpha-1,3 glycosidic linkages involved in: the expression of Lewis X/SSEA-1 and VIM-2 antigens.
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound form in trans cisterna of Golgi.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long; IsoID=Q11127-1; Sequence=Displayed;
CC Name=Short; IsoID=Q11127-2; Sequence=VSP_001778;
CC -!- TISSUE-SPECIFICITY: HIGHEST EXPRESSION IN STOMACH AND COLON. IT ALSO EXPRESSED IN THE LUNG, TESTIS, JTERUS, SMALL INTESTINE AND TO A LESSER EXTENT IN SPLEEN, AND OVARY. PRESENT IN TRACE AMOUNTS IN BRAIN, THYMUS, HEART, SMOOTH MUSCLE, KIDNEY AND BONE MARROW. NOT FOUND IN LIVER, SALIVARY GLAND AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 10.

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DR EMBL; U33457; AAC52269.1;
DR EMBL; D63380; BAA09697.1;
DR EMBL; D63379; BAA09696.1;
DR PIR; A57596; A57596;
DR MGD; MGI:95594; Futz4;
DR InterPro; IPR01503; Glyco_trans_10;
DR Pfam; PFC0852; Glyco_transf_10_1;
KW Transferase; Glycosyltransferase; Transmembrane; Glycoprotein;
KW Signal-anchor; Golgi stack; Alternative Splicing;
FT DOMAIN 1 52 CYTOPLASMIC (POTENTIAL);
FT TRANSMEM 53 74 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 75 433 (POTENTIAL);
FT CARBOHYD 117 117 LUMINAL, CATALYTIC (POTENTIAL).
FT CARBOHYD 218 218 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 1 33 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MISSING (in isoform Short).
FT /FTID=VSP_001778;
FT CONFLICT 252 252 Q -> P (IN REF. 2).
FT CONFLICT 257 257 R -> Q (IN REF. 2).
FT CONFLICT 260 260 V -> E (IN REF. 2).
FT CONFLICT 273 273 R -> Q (IN REF. 2).
SQ SEQUENCE 433 AA; 49481 MW; 2401822F02B5D021 CRC64;
Query Match 35.7%; Score 48.5; DB 1; Length 433;

Best Local Similarity 36.8%; Pred. No. 13;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 7 RLPKGYKHLKDFPILPGEI 25
| : | : | : | : | : |
Db 178 QIPVVDYSELKDYSLFPGQV 196

RESULT 10
DPO2_MOUSE STANDARD; PRT; 600 AA.
ID DPO2_MOUSE
AC P33611;
DT 01-FEB-1994 (Rel. 28, Created)

RP SEQUENCE FROM N.A.
STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;

RX RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitz E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens K., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonpre B.,
RA Weltjens I., Vanstreels E., Rieger M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880(2002).

CC !- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.
CC !- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate - glycine +
CC H(2)O - tetrahydrofolate + L-serine.

CC !- COFACTOR: Pyridoxal phosphate (BY similarity).
CC !- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS,
CC HORMONES AND OTHER COMPONENTS.
CC !- SUBUNIT: Homotrimer (BY similarity).
CC !- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC !- SIMILARITY: BELONGS TO THE SHMT FAMILY.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; Z98601; CAB11269.1; - .
CC DR PIR; T38353; T38353.
CC DR RSSP; P07511; ICJ0.
CC DR GenDB_SPombe; SPAC24C9.12C; - .
CC DR InterPro; IPR001085; Gly_HyMettransf.
CC DR Pfam; PF00464; SHMT; 1 .
CC DR PROSITE; PS00096; SHMT; 1 .
CC DR Transferase; Pyridoxal phosphate; One-carbon metabolism.
CC KW BINDING 243 243 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC FT DOMAIN 238 241 POLY-THR.
CC SQ SEQUENCE 467 AA; 51861 MW; 0C21D7EF010C3725 CRC64;

Query Match 33.8%; Score 46; DB 1; Length 467;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 10; Conservative 1; Mismatches 11; Indels 0; Caps 0;

QY 3 NYSRRLPKGVHLKDFPILPGEI 25
Db 279 SYGAQIPVDSLKEYSLFPQV 301

RESULT 11
GLYD_SCHPO STANDARD; PRT; 467 AA.
ID GLYD_SCHPO STANDARD; PRT; 467 AA.
AC 013972;
DT 15-JUL-1998 (Rel. 36, Created);
DT 15-JUL-1998 (Rel. 36, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable serine hydroxymethyltransferase, cytosolic (EC 2.1.2.1.)
DE (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT).
GN SPAC24C9.12C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
NCBI_TaxID=4896;
[1]

RESULT 12
UBIG_XYLFA STANDARD; PRT;
ID UBIG_XYLFA STANDARD; PRT;
AC Q9PAM5;
DT 28-FEB-2003 (Rel. 41, Created)

RESULT 14

MURA_SYN3	ID	MURA_SYN3	STANDARD;	PRT;	438 AA.
AC	Q55673;	DT	01-NOV-1997 (Rel. 35, Created)	RN	
	DT	01-NOV-1997 (Rel. 35, Last sequence update)	RP	SEQUENCE FROM N.A.	
	DT	28-FEB-2003 (Rel. 41, Last annotation update)	RX	MEDLINE=96379747; PubMed=8787760;	
DE	JDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)	RA	Ramos J.W.; Whittaker C.A.; Desimone D.W.;		
DE	(Enoylpyruvate) (UDPP-N-acetylglucosamine enopyruvy	RT	*Integrin-dependent adhesive activity is spatially controlled by		
DE	transferase) (EPT).	RT	"Integrin alpha-4 precursor (Integrin alpha-IV) (VLA-4).		
GN	MURA OR MUR2 OR SLR0017.	RL	Xenopus laevis (African Clawed frog)		
OS	Synechocystis sp. (strain: PCC 6803);	RN	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.	RN	OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;		
OX	NCBI_TAXID=1148;	RN	OC Xenopodinae; Xenopus.		

[1]

SEQUENCE FROM N.A.

RP MEDLINE=94008528; PubMed=8404528;

RA Whittaker C.A., Desimone D.W.;

RT RT

RT Xenopus embryos. "Integrin alpha subunit mRNAs are differentially expressed in early

RL Development 122:2873-2883(1996).

[2]

RP SEQUENCE OF 308-379 FROM N.A.

RX MEDLINE=94008528; PubMed=8404528;

RA Whittaker C.A., Desimone D.W.;

RT RT

RT Xenopus embryos. "Integrin alpha subunit mRNAs are differentially expressed in early

RL Development 117:1239-1249(1993).

CC !-- FUNCTION: FIBRONECTIN AND V-CAM ADHESION RECEPTOR.

CC !-- SUBUNIT: Heterodimer of an alpha and a beta subunit.

CC !-- SUBCELLULAR LOCATION: Type I membrane protein.

CC !-- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

CC !-- SIMILARITY: Contains 7 FG-GAP repeats.

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CC

CC DR U54497; AAA98673.1;

CC DR EMBL; L10188; AAA16248.1; -.

CC DR PIR; I51526; I51526.

CC DR HSSP; P11215; I1A8X.

CC DR InterPro; IPR000413; Integrin_alpha.

CC DR Pfam; PF01839; FG-GAP; 3.

CC DR Pfam; PF003357; integrin_A; 1.

CC DR PRINTS; PRO1185; INTEGRINA.

CC DR SMART; SM00191; Int_alpha; 5.

CC DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.

CC DR Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Repeat.

CC SIGNAL 1 34

CC FT CHAIN 35 1032

CC FT DOMAIN 35 974

CC FT TRANSMEM 975 998

CC FT DOMAIN 999 1032

CC FT REPEAT 50 112

CC FT REPEAT ? ?

CC FT REPEAT 197 247

CC FT REPEAT 248 301

CC FT REPEAT 303 361

CC FT REPEAT 364 423

CC FT REPEAT 426 474

CC FT CA_BIND 314 322

CC FT CA_BIND 376 384

CC FT CA_BIND 438 446

CC FT SITE 591 591

CC FT SITE 1001 1005

CC FT DISULFID 91 101

CC FT DISULFID 144 165

CC FT DISULFID 183 198

Query Match 33.5%; Score 45.5; DB 1; Length 554;

Best Local Similarity 41.7%; Pred. No. 35; Indexis 1; Caps 1;

Matches 10; Conservative 9; Mismatches 9; Indelis 1; Gaps 1;

Query Match 33.1%; Score 45; DB 1; Length 438;

Best Local Similarity 47.8%; Pred. No. 32; Mismatches 7; Indexis 2; Caps 1;

Matches 11; Conservative 3; Mismatches 3; Indelis 2; Caps 1;

Query Match 5 SRRRLPKGVK--HLKDFPILPGEI 25

Best Local Similarity 47.8%; Pred. No. 32; Mismatches 7; Indexis 2; Caps 1;

Matches 11; Conservative 3; Mismatches 3; Indelis 2; Caps 1;

DB 228 SRIINGVEKLHSTDFFPIIPDRI 25C

	FT	DISULFID	494	BY SIMILARITY.
	FT	DISULFID	500	BY SIMILARITY.
	FT	DISULFID	556	BY SIMILARITY.
	FT	DISULFID	622	BY SIMILARITY.
	FT	DISULFID	627	BY SIMILARITY.
	FT	DISULFID	698	BY SIMILARITY.
	FT	DISULFID	712	BY SIMILARITY.
	FT	DISULFID	853	BY SIMILARITY.
	FT	DISULFID	889	BY SIMILARITY.
	FT	CARBOHYD	901	BY SIMILARITY.
	FT	CARBOHYD	81	N-LINKED (GLCNAC).
	FT	CARBOHYD	98	N-LINKED (GLCNAC).
	FT	CARBOHYD	229	N-LINKED (GLCNAC).
	FT	CARBOHYD	479	N-LINKED (GLCNAC).
	FT	CARBOHYD	496	N-LINKED (GLCNAC).
	FT	CARBOHYD	517	N-LINKED (GLCNAC).
	FT	CARBOHYD	537	N-LINKED (GLCNAC).
	FT	CARBOHYD	626	N-LINKED (GLCNAC).
	FT	CARBOHYD	660	N-LINKED (GLCNAC).
	FT	CARBOHYD	746	N-LINKED (GLCNAC).
	FT	CARBOHYD	857	N-LINKED (GLCNAC).
SQ	SEQJENCE	1032	AA:	115215 MW: 6486797D33AAE69E CRC64;
Query Match 33.18; Score 45; DB 1; Length 2032;				
Best Loca: Similarity 52.68; Pred. No. 83;				
Matches 10; Conservative 3; Mismatches 6; Indexes 0; Ca				
Qy	7	RLPKGVKHLKDFPILLPGEI	25	
	!	! : - : !		
Db	678	RLPKGLYFVKVFDLLEKEI	696	

Search completed: October 17, 2003, 11:33:39
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: October 17, 2003, 11:33:11 ; search time 95 seconds
 (without alignments)
 67.909 Million cell updates/sec

Title: SEQID2-NAT3
 Perfect score: 136
 Sequence: 1 RPNSRRLPKGVKHLKDFPILPGEI 25

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 83C525

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : SP:TREMBL_23:^{*}

1: sp_archaea:^{*}
 2: sp_bacteria:^{*}
 3: sp_fungi:^{*}
 4: sp_human:^{*}
 5: sp_invertebrate:^{*}
 6: sp_mammal:^{*}
 7: sp_mhc:^{*}
 8: sp_organelle:^{*}
 9: sp_phage:^{*}
 10: sp_plant:^{*}
 11: sp Rodent:^{*}
 12: sp_virus:^{*}
 13: sp_vertebrate:^{*}
 14: sp_unclassified:^{*}
 15: sp_rvirus:^{*}
 16: sp_bacteriopl:^{*}
 17: sp_archeap:^{*}

17 48.5 35.7 386 11 Q920V9
 18 48.5 35.7 390 11 Q91V20
 19 48.5 35.7 390 11 Q920V7
 20 48.5 35.7 390 11 Q920V6
 21 48.5 35.7 390 11 Q920W1
 22 48.5 35.7 390 11 Q920W0
 23 48.5 35.7 390 11 Q91VB5
 24 48.5 35.7 390 11 Q920V8
 25 48.5 35.7 1253 10 Q8RYK8
 26 48.5 35.7 1253 10 Q9SC23
 27 48 35.3 55 7 Q9MWB4
 28 48 35.3 156 16 Q9HXF9
 29 48 35.3 264 16 Q8YKJ6
 30 48 35.3 360 11 Q922M1
 31 48 35.3 454 11 Q8CIL1
 32 48 35.3 566 11 Q8C2T6
 33 48 35.3 600 11 Q8VDR3
 34 48 35.3 600 11 Q9QYV6
 35 48 35.3 1161 10 Q9LRZ0
 36 48 35.3 1690 3 Q74835
 37 47.5 34.9 350 2 Q93F54
 38 47.5 34.9 352 2 Q93F60
 39 47.5 34.9 352 2 Q93F48
 40 47.5 34.9 401 11 Q9JIK2
 41 47.5 34.9 433 11 Q99N88
 42 47 34.6 187 16 Q82MP8
 43 47 34.6 345 16 Q8NLX9
 44 47 34.6 444 10 Q43756
 45 47 34.6 537 16 Q8E9K6

ALIGNMENTS

RESULT 1
 ID 062730 PRELIMINARY; PRT; 2343 AA.
 AC 062730; ID 062730; PRELIMINARY;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Factor VIII.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Spleen;
 RA Gordy P.W.; Bowen R.A.;
 RT "Characterization of the canine factor VIII cDNA."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 CC !- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
 EMBL: AF049489; AAC05384.1; -.
 DR HSSP; P00451; ICFG.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR000421; FA58_C.
 DR Pfam; PF00394; Cu-oxidase; 3.
 DR Pfam; PF00394; F5_F8-type_C; 2.
 DR SMART; SM00231; FA58_C.
 DR PROSITE; PS01285; FA58_C_1; 2.
 DR PROSITE; PS01286; FA58_C_2; 2.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
 SQ SEQUENCE 2343 AA; 265613 MW; F612D744ADAADD99 CRC64;
 Query Match 74.3%; Score 101; DB 6; Length 2343;
 Best Local Similarity 79.2%; Pred. No. 3.3e-06;
 Matches 19; conservative 2; Mismatches 3; Indels 0; Gaps 0;

8

Result No.	Query	Score	Match	Length	DB	ID	Description
1	101	74.3	2343	6	062730	C62730 canis familiaris	
2	101	74.3	2343	6	062730	018806 canis familiaris	
3	53.5	39.3	611	16	Q8EYK8	08EYK8 leptospira	
4	51.5	37.9	911	16	Q8DACS	08dacs vibrio vulnificus	
5	51	37.5	166	4	Q96AX6	096ax6 homo sapiens	
6	51	37.5	907	16	Q8DLH3	08dlh3 synechococcus	
7	51	37.5	1607	10	065506	065506 arabiopsis thaliana	
8	50.5	37.1	589	2	Q9S158	09s158 comamonas tenebrionis	
9	50.5	37.1	935	5	Q9VE79	09ve79 drosophila melanogaster	
10	50	36.8	388	10	Q8SAW1	08saw1 oryza sativa	
11	50	36.8	579	4	Q96A81	096a81 homo sapiens	
12	50	36.8	706	10	Q8S5J1	08s5j1 oryza sativa	
13	50	36.8	958	16	Q9PBAT	09pbat xylophaga	
14	50	36.8	2618	5	Q9VPB8	09vpb8 drosophila	
15	49	36.0	412	17	Q58994	058994 pyrococcus	
16	49	36.0	986	10	Q8GRU6	08gru6 lotus japonicus	

RESULT 2	ID 018806 PRELIMINARY; PRT; 2343 AA.	Q8DACS5 ID Q8DACS5 PRELIMINARY; PRT; 911 AA.
AC 018806; DT 01-JAN-1998 (TREMBLrel. 05, Created)	AC 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	AC 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DE GGDEF family protein.	DE GGDEF family protein.
DE Factor VIII.	GN VV12281.	GN VV12281.
GN F8.	OS Vibrio vulnificus.	OS Vibrio vulnificus.
OS Canis familiaris (Dog).	OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Vibriaceae; Vibrio.	OC Vibriaceae; Vibrio.
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	OX NCBI_TAXID=9615;	OX NCBI_TAXID=672;
OX NCBI_TAXID=9615;	RN [1]	RN [1]
RN	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC TISSUE-Liver;	RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	RC STRAIN=CMCP6;
RA Cameron C., Notley C., Hoyle S., McClynn L., Hough C., Kamisue S., Giles A., Lillincrap D.; RT "The canine factor VIII cDNA and 5' flanking sequence.";	RA Choy H.E., RT "Complete genome sequence of <i>Vibrio vulnificus</i> CMCP6."	RA Choy H.E., RT "Complete genome sequence of <i>Vibrio vulnificus</i> CMCP6."
RA Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.	RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC -!-. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.	DR EMBL; AE016804; AAO10659.1; -.	DR EMBL; AE016804; AAO10659.1; -.
DR EMBL; AF016234; PAB87412.i; -.	SQ SEQUENCE 911 AA; 103424 MW; 23D2868E85D3AEFD CRC64;	SQ SEQUENCE 911 AA; 103424 MW; 23D2868E85D3AEFD CRC64;
DR HSSP; PC0451; ICRG.	Query Match 37.9%; Score 51.5%; Pred. No. 44;	Query Match 37.9%; Score 51.5%; Pred. No. 44;
DR InterPro; IPR001117; Cu-oxidase.	Best Local Similarity 43.5%; Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;	Best Local Similarity 43.5%; Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
DR InterPro; IPR00421; FA58_C.	Qy 4 YSRRLPKGVKHLKD-FPILPGEI 25	Qy 4 YSRRLPKGVKHLKD-FPILPGEI 25
DR Pfam; PF00394; Cu Oxidase; 3.	DR SMART; SM00231; FA58C; 2.	DR SMART; SM00231; FA58C; 2.
DR Pfam; PF00754; F5_F8_type_C; 2.	DR PROSITE; PS01285; FA58C_1; 2.	DR PROSITE; PS01286; FA58C_2; 2.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.	DR PROSITE; PS01286; FA58C_2; 2.	DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.	DR PROSITE; PS01286; FA58C_2; 2.	DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
SQ SEQUENCE 2343 AA; 265829 MW; A854FAE571C3B399 CRC64;	DR PROSITE; PS01286; FA58C_2; 2.	DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 3.
Query Match 74.3%; Score 101; DB 6; Length 2343;	Qy 2 PNYSRRLPKGVKHLKDFFPILPGEI 25	Qy 2 PNYSRRLPKGVKHLKDFFPILPGEI 25
Best Local Similarity 79.2%; Pred. No. 3.3e-06;	Best Local Similarity 79.2%; Mismatches 3; Indels 0; Gaps 0;	Best Local Similarity 79.2%; Mismatches 3; Indels 0; Gaps 0;
Matches 19; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Db 498 PLHTGRJPKGVKHLKDMPILPGEI 521	Db 498 PLHTGRJPKGVKHLKDMPILPGEI 521
Qy 2 PNYSRRLPKGVKHLKDFFPILPGEI 25	DR 521	DR 521
Db 498 PLHTGRJPKGVKHLKDMPILPGEI 521	RA Ren S.; SL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.	RA Ren S.; SL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RA Ren S.; SL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.	DT EMBL; AE011574; AAN51406.1; -.	DT EMBL; AE011574; AAN51406.1; -.
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DE Conserved hypothetical protein.	DE Conserved hypothetical protein.
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	GN LA4208.	GN LA4208.
DE Conserved hypothetical protein.	OS Leptospira interrogans.	OS Leptospira interrogans.
GN LA4208.	Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.	Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OS Leptospira interrogans.	OX NCBI_TAXID=173;	OX NCBI_TAXID=173;
OX NCBI_TAXID=173;	RN [1]	RN [1]
RN SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Scrovar lai;	RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Scrovar lai;	RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Scrovar lai;
RA Ren S.; SL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.	DR EMBL; AE011574; AAN51406.1; -.	DR EMBL; AE011574; AAN51406.1; -.
DR EMBL; AE011574; AAN51406.1; -.	KW Hypothetical Protein; Complete proteome.	KW Hypothetical Protein; Complete proteome.
KW Hypothetical Protein; Complete proteome.	SEQUENCE 611 AA; 69435 MW; 4055F7B88D91594C CRC64;	SEQUENCE 611 AA; 69435 MW; 4055F7B88D91594C CRC64;
SEQUENCE 611 AA; 69435 MW; 4055F7B88D91594C CRC64;	Query Match 39.3%; Score 53.5%; Pred. No. 14;	Query Match 39.3%; Score 53.5%; Pred. No. 14;
Best Local Similarity 52.2%; Mismatches 3; Indels 3; Gaps 2;	Best Local Similarity 52.2%; Mismatches 3; Indels 3; Gaps 2;	Best Local Similarity 52.2%; Mismatches 3; Indels 3; Gaps 2;
Matches 12; Conservative 5; Mismatches 3; Indels 3; Gaps 2;	Qy 6 RRLP-KGV-KHLKDFFPILPGEI 25	Qy 6 RRLP-KGV-KHLKDFFPILPGEI 25
Db 450 KRYPLIKGIFKNVGFFPILPGEV 472	Db 450 KRYPLIKGIFKNVGFFPILPGEV 472	Db 450 KRYPLIKGIFKNVGFFPILPGEV 472
RESULT 4	Q8DLH3 ID Q8DLH3 PRELIMINARY; PRT; 907 AA.	RESULT 6
AC Q8DACS5; DT 01-MAR-2003 (TREMBLrel. 23, Created)	AC Q8DACS5; DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	AC Q8DLH3; DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	DE GGDEF family protein.	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE GGDEF family protein.	GN VV12281.	DE T110519 protein.
GN VV12281.	GN TLL0519.	GN TLL0519.

OS Synechococcus elongatus (Thermosynechococcus elongatus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TAXID=32046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BP-1;
 RX MEDLINE-22225144; PubMed-12240834;
 RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriuchii M., Kawashima K., Kimura T., Kishida Y., RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., RA Skimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; RT "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
 RT DNA Res. 9:123-130(2002);
 RL EMBL; AP005370; BAC08071.1; -.
 DR KW Complete proteome;
 SQ SEQUENCE 907 AA; 101695 MW; 30DFFEE9B368A775 CRC64;

Query Match 37.58; Score 51; DB 16; Length 907;
 Best Local Similarity 37.58; Pred. No. 52;
 Matches 9; Conservative 5; Mismatches 10; Indels 9; Gaps 0;

RESULT 8
 ID 065506 PRELIMINARY; PRT; 1607 AA.
 AC 065506;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative disease resistance protein.
 CN F23E13.30 OR AT4G36140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TAXID=3702;
 RN SEQUENCE FROM N.A.
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duysterhoef A., RA Hoheisel J., Jesse T., Heinen L., Vos P., Mewes H.W., Mayer K., RA Schueler C.; Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 RN SEQUENCE OF 1448-1607 FROM N.A.
 RA Bevan M., Wedler H., Wambutt R., Hoheisel J., Jesse T., Heijnen L., RA Vos P., Mewes H.W., Mayer K., Schueler C.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 1421-1607 FROM N.A.
 RA Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.; RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN SEQUENCE FROM N.A.
 RA Hilbert H., Braun M., Holzer E., Brandt A., Duysterhoef A., RA Mewes H.W., Lemcke K., Mayer K.F.X.; RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL022141; CAA18120.1; -.
 DR EMBL; AL022373; CAA18508.1; -.
 DR EMBL; AL161588; CAB81523.1; -.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR InterPro; IPR000157; TIR_domain.

DR Pfam; PF00560; LRR; 3.
 DR Pfam; PF00931; NB-ARC; 2.
 DR Pfam; PF01582; TIR; 2.
 DR PRINTS; PRO00364; DISSEASERIST.
 DR SMART; SM00382; AAA; 2.
 DR SMART; SM00255; TIR; 2.
 DR PROSITE; PS50104; TIR; 1.
 DR ATP-binding.
 KW ATP-binding.
 SQ SEQUENCE 1607 AA; 182785 MW; 4F8F572EC72074F3 CRC64;

Query Match 37.58; Score 51; DB 10; Length 1607;
 Best Local Similarity 66.78; Pred. No. 97;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 9
 ID Q9VE79 PRELIMINARY; PRT; 935 AA.
 AC Q9VE79;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG14309 protein.

Query Match 37.18; Score 50.5; DB 2; Length 589;
 Best Local Similarity 41.78; Pred. No. 38;
 Matches 10; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

RESULT 10
 ID 218 RPYVSAALPHGIRRF-EFMVMPGE 240
 DR RPYVSAALPHGIRRF-EFMVMPGE 240

CG14309.	Drosophila melanogaster (Fruit fly).	
DS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
DC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
DC	Ephydrioidea; Drosophilidae; Drosophila.	
NCBI_TAXID=7227;		
[1]	SEQUENCE FROM N.A.	
STRAIN-BERKELEY;	MEDLINE-20196006; PubMed-1C731132;	
RX	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gaile R.F., George R.A., Lewis S.E., Richards S.N., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo C., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Duan P., Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmaan W., Fosler C., Gabrielian A.E., Gong F., Gorrell J.H., Gu Z., Guan P., Gelbart W.M., Giasser K., Gloedek A., Harris N.L., Harvey D., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Heiman T.J., Kibegwan C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Leib Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Moberry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Neilsen D.L., Neison D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Sher H., Shue B.C., Siden-Kiamos I., Simpson M.P., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000). EMBL: AE003721; AAF55548.1; FlyBase: FBgn0038611; CG14309. SEQUENCE 935 AA; 106833 MW;	
RN	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.	
RC	InterPro; IPR000152; Asx_hydroxyl.	
RX	Gramene; Q8SAW1; -.	
RA	Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T., Sasaki C., Henry D., Oates R., Simmons J.;	
RA	*Rice Genomic Sequence."	
RT	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.	
RL	DR EMBL; AC09B566; AAL77114.1; -.	
DR	InterPro; IPR000152; Asx_hydroxyl.	
DR	DR InterPro; IPR001881; EGF_Ca.	
DR	DR SMART; SM00179; EGF_Ca; 1.	
DR	DR PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	DR PROSITE; PS01187; EGF_Ca; 1.	
KW	EGF-like domain; Kinase.	
SQ	SEQUENCE 388 AA; 42179 MW; 0F4F47E6F087FF91 CRC64;	
Query Match	36.8%; Score 50; DB 10; Length 388;	
Best Local Similarity	47.6%; Pred. No. 29;	
Matches	1C; Conservative 4; Mismatches 7; Indels 0; Gaps 0;	
Oy	3 NYSSRLPKGVKHLKDFPILPG 23 : : : : : 240 NFSKKYPKGVPLVIDFAIRDG 260	
Db		
RESULT 11		
Q96A81	PRELIMINARY; PRT; 579 AA.	
ID	Q96A81	
AC	Q96A81;	
DT	01-DEC-2001 (TREMBLrel. 19, created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
ST	Hypothetical protein FLJ31952.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TAXID=9606;	
RN		
RP	SEQUENCE FROM N.A.	
RA	Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takanashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuoka K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami S., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEEDO human cDNA sequencing project.";	
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	
DR	DR AK056514; BAB71201.1; -.	
KW	Hypothetical protein.	
SQ	SEQUENCE 579 AA; 65949 MW; 195AEFB2F4235C84 CRC64;	
Query Match	36.8%; Score 50; DB 4; Length 579;	
Best Local Similarity	40.0%; Pred. No. 45;	
Matches	5; Conservative 5; Mismatches 5; Indels 8; Gaps 2;	
Oy	1 RPNNYSRRRLPKGVKHLKD----FPILPGEI 25 : : : : : : 575 PTYT-RLPEDDVHLKHETVDGEV 597	
Db	61 RPVYSK--KGLEHKADLQQHLPVPPGHL 87	
RESULT 12		
Q8SAW1	PRELIMINARY; PRT; 368 AA.	
ID	Q8SAW1;	
AC	Q8SAW1;	
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
PUTATIVE WALL-ASSOCIATED PROTEIN KINASE.	PUTATIVE WALL-ASSOCIATED PROTEIN KINASE.	
OSJNBA0051J07.1	OSJNBA0051J07.1	
Oryza sativa (Rice).	Oryza sativa (Rice).	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
GN	OSJNBA001A24.33.	

OS *Oryza sativa* (Japonica cultivar-group); Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBITaxID=39947;
 OX [1])
 RN SEQUENCE FROM N.A.
 RP STRAIN=CV. Nippobare:
 RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
 RA Kuit K., Nascenti L., Zutavern T., Ballija V., Bell M., Baker J.,
 RA Santos L., Miller B., Katzenberger F., Mulier S., King L., Yang C.,
 RA Dike S., O'Shaughnessy A., Palmer L., Dechka N.;
 RA "Genomic sequence for *Oryza sativa*, Nipponbare strain, clone CSJNBA0011A24, from chromosome 10, complete sequence.";
 RT Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 RL EMBL; AC113336; AAM01181.i; -.
 DR InterPro; Q8SS5G1;
 DR InterPro; IPR000152; ASX_hydroxy1.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR000719; Prot_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD0000061; Prot_kinase; 1.
 DR SMART; SM00179; EGF_Ca; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS550011; PROTEIN_KINASE_DCM; 1.
 DR ATP-binding; EGF-like domain; Kinase; Transcrase.
 KW SEQUENCE 706 AA; 77555 MW; 911E6F07E9B90BFE8 CRC64;
 SQ

Query Match: 36.8%; Score: 50; DB: 10; Length: 706;
 Best Local Similarity: 47.6%; Pred. No.: 56;
 Matches: 10; Conservative: 4; Mismatches: 7; Indels: 0; Gaps: 0;

DE Hypothetical protein Xf2237.

GN OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylellida.
 NCBI_TaxID=2371;

RESULT 13

Q9PBAA7 ID Q9PBAA7 PRELIMINARY; PRT; 958 AA.
 AC Q9PBAA7;
 DT 01-OCT-2000 (TREMBLrel: 15, Created)
 DT 01-MAR-2003 (TREMBLrel: 23, Last annotation update)
 DE Hypothetical protein Xf2237.

GN OS *Xylella fastidiosa*.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylellida.
 NCBI_TaxID=2371;

[1])
 RN SEQUENCE FROM N.A.
 RP STRAIN=945C;
 RC MEDLINE=20365717; PubMed=10910347;
 RX Simpson A.J.G., Reinach F.C., Arreda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonacorsini E.D., Bordim S., Braga J.M., Britto M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrara D.M., Carrer H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferrc J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Froehne M., Furian L.R.,
 RA Garnier M., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Macleod J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.Z.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., dc Rosa A.J.M.,
 RA da Rosa V.E. Jr., de Sa R.G., Santelli R., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovskii-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RI "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
 RL Nature 406:151-159 (2000).
 DR EMBL; AE004036; AAF85036.1;
 DR InterPro; IPR000531; TonB_boxC;
 DR Pfam; PF00593; TonB_dep_rec; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 958 AA; 103030 MW; 4EF720E00D333EDB CRC64;

RESULT 14

Q9VP68 ID Q9VP68 PRELIMINARY; PRT; 2618 AA.
 AC Q9VP68; Q9N6F9;
 DT 01-MAY-2000 (TREMBLrel: 13, Created)
 DT 01-OCT-2002 (TREMBLrel: 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel: 22, Last annotation update)
 DE CG9936 protein (JLKJLKJ) (TRAP240) (PAP/DTRAP240) (Transcriptional coactivator BLIND spot).
 DE GN PAP OR BLI OR CG9936.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydrioidea; Drosophilidae; Drosophila.
 OC NCBI_TAXID=7227;
 OX RN

[1])
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkeley;
 RC MEDLINE=20196006; PubMed=10731132;
 RX Adams M.D., Celniker S.E., Holt R.A., Gocayne J.D.,
 RA Amanatides P.G., Scheerer S.E., Li P.W., Roskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abri J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bhandari P.,
 RA Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrilian A.E., Garg N.S., Gelman W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purji V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., DR EMBL; AF227215; AAF43172.1; -.

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., DR EMBL; AF226855; AAF36691.1; -.

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., DR EMBL; AF227214; AAF43021.1; -.

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., DR EMBL; AF324425; AAG48327.1; -.

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yac Q.A., DR FLYBase; FBgn0024200; pap.

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., SQ SEQUENCE 2618 AA; 280021 MW; 735A8A502076844E CRC64;

RA Gibbs R.A., Myers E.W., Rubin G.M., Rubin J.C.; DR Query Match 36.88; Score 50; DB 5; Length 2618;

RA "The genome sequence of *Drosophila melanogaster*,"; RT Best Local Similarity 40.98; Pred. No. 2.4e+02;

RA Science 287:2185-2195 (2000). RT Matches 9; Conservative 6; Mismatches 5; Indels 2; Gaps 1;

RL RN

SEQUENCE FROM N.A.

RA Celiker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., DR EMBL; AF227215; AAF43172.1; -.

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., DR EMBL; AF227214; AAF43021.1; -.

RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., DR EMBL; AF227213; AAF43020.1; -.

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., DR EMBL; AF227212; AAF43019.1; -.

RA Dodson K., Dorsett V., Douc L.E., Doyle C., Dressnek D., Farfan D., DR EMBL; AF227211; AAF43018.1; -.

RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., DR EMBL; AF227210; AAF43017.1; -.

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., DR EMBL; AF227209; AAF43016.1; -.

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Mosherefi A., DR EMBL; AF227208; AAF43015.1; -.

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., DR EMBL; AF227207; AAF43014.1; -.

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., DR EMBL; AF227206; AAF43013.1; -.

RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., DR EMBL; AF227205; AAF43012.1; -.

RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D., DR EMBL; AF227204; AAF43011.1; -.

RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; DR EMBL; AF227203; AAF43010.1; -.

RT "Sequencing of *Drosophila melanogaster* genome,"; RT Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RL RN

SEQUENCE FROM N.A.

RA Misra S., Crosby M.A., Matthews B.Z., Bayraktaroglu L., Campbell K., DR EMBL; AF227202; AAF43009.1; -.

RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., DR EMBL; AF227201; AAF43008.1; -.

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celtniker S.E., DR EMBL; AF227200; AAF43007.1; -.

RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., DR EMBL; AF227199; AAF43006.1; -.

RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., DR EMBL; AF227198; AAF43005.1; -.

RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., DR EMBL; AF227197; AAF43004.1; -.

RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; DR EMBL; AF227196; AAF43003.1; -.

RA "Annotation of *Drosophila melanogaster* genome,"; DR EMBL; AF227195; AAF43002.1; -.

RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RL RN

SEQUENCE FROM N.A.

RA Adams M.D., Celtniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; DR EMBL; AF227194; AAF43001.1; -.

RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RL RN

SEQUENCE FROM N.A.

RA Flybase; DR Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

RL RN

SEQUENCE FROM N.A.

RA Boube M., Faucher C., Joulia L., Cribbs D.L., Bourbon H.M.; DR EMBL; AF227193; AAF43000.1; -.

RA "The *Drosophila* Mediator proteins DTRAP240 and DTRAP80 are transcriptional cofactors of the proboscipedia and Sex combs reduced homeotic proteins,"; DR EMBL; AF227192; AAF42999.1; -.

RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

RL RN

SEQUENCE FROM N.A.

RA Nairz K., Hafen E.; DR EMBL; AF227191; AAF42998.1; -.

RT "Isolation of flytrap (pap), the *Drosophila* TRAP240 homologue,"; DR EMBL; AF227190; AAF42997.1; -.

RL RN

SEQUENCE FROM N.A.

RA Boube M., Faucher C., Joulia L., Cribbs D.L., Bourbon H.M.; DR EMBL; AF227189; AAF42996.1; -.

RT "The *Drosophila* Mediator proteins DTRAP24C and DTRAP80 are transcriptional cofactors of the proboscipedia and Sex combs reduced homeotic proteins,"; DR EMBL; AF227188; AAF42995.1; -.

RT Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

RL RN

SEQUENCE FROM N.A.

RA Treisman J.E.; DR EMBL; AF227187; AAF42994.1; -.

RT "Drosophila homologs of the transcriptional coactivation complex subunits TRAP240 and TRAP230 are required for identical processes in eye-antennal disc development,"; DR EMBL; AF227186; AAF42993.1; -.

RT Development 0:0-0(2001); DR EMBL; AE003593; AAF51667.2; -.

RL DR

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OM protein - protein search, using sw model

Run on: October 17, 2003, 11:33:45 ; Search time 30 Seconds
(Without alignments;
35.259 Million cell updates/sec)

Title: SEQID2-NAT3
Perfect score: 136
Sequence: 1 RPnYSRRLPKGVHLKDFPILPGEI 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310856 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%,
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgtn2_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cgtn2_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cgtn2_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cgtn2_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cgtn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
 6: /cgtn2_6/ptodata/1/iaa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	127	93.4	1438	4 US-09-209-916-1	Sequence 1, Appli
2	127	93.4	1471	1 US-08-683-839B-3	Sequence 3, Appli
3	127	93.4	1661	2 US-08-882-083-2	Sequence 2, Appli
4	127	93.4	1661	2 US-08-558-107-2	Sequence 2, Appli
5	127	93.4	1661	3 US-09-243-539-2	Sequence 2, Appli
6	127	93.4	2332	1 US-07-864-004B-4	Sequence 4, Appli
7	127	93.4	2332	1 US-08-251-937A-4	Sequence 4, Appli
8	127	93.4	2332	1 US-08-212-133A-2	Sequence 2, Appli
9	127	93.4	2332	1 US-08-276-594A-2	Sequence 2, Appli
10	127	93.4	2332	1 US-08-474-503-2	Sequence 2, Appli
11	127	93.4	2332	2 US-08-670-707A-2	Sequence 2, Appli
12	127	93.4	2332	3 US-09-037-601-2	Sequence 2, Appli
13	127	93.4	2332	3 US-09-324-867-3	Sequence 3, Appli
14	127	93.4	2332	4 US-09-315-179-2	Sequence 2, Appli
15	127	93.4	2332	4 US-09-523-656-2	Sequence 2, Appli
16	127	93.4	2332	5 PCT-US93-03275-4	Sequence 4, Appli
17	127	93.4	2332	5 PCT-US94-13200-2	Sequence 2, Appli
18	127	93.4	2351	1 US-08-121-202-2	Sequence 2, Appli
19	127	93.4	2351	1 US-08-366-851A-2	Sequence 2, Appli
20	127	93.4	2351	6 5171844-2	Patent No. 5171844
21	127	93.4	2351	6 5422260-1	Patent No. 5422260
22	101	74.3	2343	3 US-09-324-867-2	Sequence 4, Appli
23	94	69.1	2304	3 US-09-324-867-4	Sequence 6, Appli
24	94	69.1	2319	1 US-08-212-133A-8	Sequence 6, Appli
25	94	69.1	2319	1 US-08-474-503-6	Sequence 6, Appli
26	94	69.1	2319	2 US-08-670-707A-6	Sequence 6, Appli
27	94	69.1	2319	3 US-09-037-601-3	Sequence 6, Appli

ALIGNMENTS

SEQ ID NO	LENGTH	TYPE: PRT	ORGANISM: Artificial sequence	FEATURE:	OTHER INFORMATION: Description of Artificial Sequence: Derived from US-09-209-916-1
1	1438	RESULT 1 US-09-209-916-1 ; Sequence 1, Application US/09209916 ; Patent No. 6358703 ; GENERAL INFORMATION: ; APPLICANT: Cho, Myung-Sam ; APPLICANT: Chan, Sham-Yuen ; APPLICANT: Kelsey, William ; APPLICANT: Yee, Helena ; TITLE OF INVENTION: Expression System for Factor VIII ; FILE REFERENCE: MSB-7255 ; CURRENT APPLICATION NUMBER: US/09/209, 916 ; CURRENT FILING DATE: 1998-12-10 ; NUMBER OF SEQ ID NOS: 2 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 1438	Query Match 93.4%; Score 127; DB 4; Length 1438; Best Local Similarity 96.0%; Pred. No. 4.3e-11; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1	RPNYSRRLPKGVKHLKDFPILPGEI 25	Qy 1 RPNYSRRLPKGVKHLKDFPILPGEI 25		
Db	484	RPLYSRRLPKGVKHLKDFPILPGEI 508	Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508		

RESULT 2
US-08-683-839B-3
; Sequence 3, Application US/08683839B
; Patent No. 5744326
; GENERAL INFORMATION:
; APPLICANT: Ill, Charles . R. et al.
; TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional Regulatory Sequences To Increase Expression Of Title Of Invention: Intronless Genes Containing Near-Consensus Splice Sites
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,839B
; FILING DATE: 11-MARCH-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: TTI-138
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1471 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-683-839B-3

Query Match          93.4%; Score 127; DB 2; Length 1471;
Best Local Similarity 96.0%; Pred. No. 5.1e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPNYSRRLPKGVKHLKDFPILPGEI 25
Db      503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 3
US-08-882-083-2
; Sequence 2, Application US/08882083
; Patent No. 5869292
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-558-107-2

Query Match          93.4%; Score 127; DB 2; Length 1661;
Best Local Similarity 96.0%; Pred. No. 5.1e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPNYSRRLPKGVKHLKDFPILPGEI 25
Db      503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 4
US-08-558-107-2
; Sequence 2, Application US/08558107
; Patent No. 5910481
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-558-107-2

Query Match          93.4%; Score 127; DB 2; Length 1661;
Best Local Similarity 96.0%; Pred. No. 5.1e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPNYSRRLPKGVKHLKDFPILPGEI 25
Db      503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 5
US-09-243-539-2
; Sequence 2, Application US/09243539
; Patent No. 6130203
; GENERAL INFORMATION:
; APPLICANT: VOORBERG, Johannes J.
; TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,107
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/558,107
; FILING DATE: 13-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 30472/212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 1661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-243-539-2

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ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3C
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/243,539
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/558,107
 FILING DATE: 13-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: ISACSON, John P.
 REGISTRATION NUMBER: 33,715
 REFERENCE/DOCKET NUMBER: 30472/2i2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1661 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-243-539-2

Query Match 93.4%; Score 127; DB 3; Length 1661;
 Best Local Similarity 96.0%; Pred. No. 5.1e-11;
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 6
 US-07-864-004B-4

Sequence 4, Application US/07864004B
 Patent No. 5364771

GENERAL INFORMATION:
 APPLICANT: Lollar, John S.
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 APPLICANT: Runge, Marschall S.
 TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
 ADDRESS: Kilpatrick & Cody
 STREET: 1100 Peachtree Street
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: US
 ZIP: 30309

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/251,937A
 FILING DATE: 31-MAY-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/864,004
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Pratt, John S.
 REGISTRATION NUMBER: 29,476
 REFERENCE/DOCKET NUMBER: EMU106DIV

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6367
 TELEFAX: 404-815-6555

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapien

; TISSUE TYPE: Liver cDNA sequence
 US-08-251-937A-4
 Query Match 93.4%; Score 127; DB 1; Length 2332;
 Best Local Similarity 96.0%; Pred. No. 7.4e-11;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 8
 US-08-212-133A-2
 ; Sequence 2, Application US/08212133A
 ; Patent No. 5663060
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S.
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kilpatrick & Cody
 ; STREET: 100 Peachtree Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/212,133A
 ; FILING DATE: March 11, 1994
 ; CLASSIFICATION: 435
 ; PRIORITY DATA:
 ; APPLICATION NUMBER: US 07/950,191
 ; FILING DATE: 24-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 243262/1991
 ; FILING DATE: 24-SEP-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.
 ; REGISTRATION NUMBER: 25,258
 ; REFERENCE/DOCKET NUMBER: 74129/195/AOPA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: EMU/76677
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-572-6508
 ; TELEFAX: 404-572-6555
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2332 amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapien
 ; TISSUE TYPE: Liver cDNA sequence
 ; US-08-212-133A-2

Query Match 93.4%; Score 127; DB 1; Length 2332;
 Best Local Similarity 96.0%; Pred. No. 7.4e-11;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508
 RESULT 9
 US-08-276-594A-2

Sequence 2, Application US/08276594A
 Patent No. 5693499
 ; GENERAL INFORMATION:
 ; APPLICANT: YONEMURA, Hiroshi
 ; APPLICANT: TAJIMA, Yoshitaka
 ; APPLICANT: SUGAWARA, Keiichi
 ; APPLICANT: MASUDA, Kenichi
 ; TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/276,594A
 ; FILING DATE: 18-JUL-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/950,191
 ; FILING DATE: 24-SEP-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 243262/1991
 ; FILING DATE: 24-SEP-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.
 ; REGISTRATION NUMBER: 25,258
 ; REFERENCE/DOCKET NUMBER: 74129/195/AOPA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2332 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; Query Match 93.4%; Score 127; DB 1; Length 2332;
 ; Best Local Similarity 96.0%; Pred. No. 7.4e-11;
 ; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 ; Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 ; Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508
 ; RESULT 10
 ; US-08-474-503-2
 ; Sequence 2, Application US/08474503
 ; Patent No. 5744446
 ; GENERAL INFORMATION:
 ; APPLICANT: Emory University/Hybrid Human/Animal Factor VIII
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kilpatrick & Cody
 ; STREET: 1100 Peachtree Street, Suite 2800
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30309
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474, 503
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Pratt, John S.
 REGISTRATION NUMBER: 29, 476
 REFERENCE/DOCKET NUMBER: EMU106CIP(3)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6500
 TELEFAX: 404-815-6555

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Liver

US-08-670-707A-2

Query Match 93.4%; Score 127; DB 1; Length 2332;
 Best Local Similarity 96.0%; Pred. No. 7.4e-11;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPNTSRLPKGVKHLKDFPILGEI 25
 Db 484 RPLYTSRLPKGVKHLKDFPILGEI 508

RESULT 12
 US-09-037-601-2
 Sequence 2, Application US/09037601
 ; Patent No. 6180371
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S.
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/037, 601
 ; FILING DATE: 26-JUN-1996
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US94/13200
 ; FILING DATE: 15-NOV-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212, 133
 ; FILING DATE: 11-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/864, 004
 ; FILING DATE: 07-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferber, Donna M.
 ; REGISTRATION NUMBER: 33, 878
 ; REFERENCE/DOCKET NUMBER: 75-95F
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 303/499-8080
 ; TELEFAX: 303/499-8089

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Liver
 US-09-037-601-2

Query Match 93.4%; Score 127; DB 3; Length 2332;
 Best Local Similarity 96.0%; Pred. No. 7.4e-11;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 13
 US-09-324-867-3
 Sequence 3, Application US/09324867A
 Patent No. 6251632
 GENERAL INFORMATION:
 APPLICANT: Lilligraf, David
 APPLICANT: Cameron, Cherie
 APPLICANT: No. 6251632ley, Colieer
 APPLICANT: Horrocks, L. Suzanne Royle
 APPLICANT: Hough, Christine
 TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
 FILE REFERENCE: 1669.001002/JAG/BJD
 CURRENT APPLICATION NUMBER: US/09/324,867A
 CURRENT FILING DATE: 1999-06-03
 EARLIER APPLICATION NUMBER: 09/035,141
 EARLIER FILING DATE: 1998-03-05
 EARLIER APPLICATION NUMBER: 60/039,953
 EARLIER FILING DATE: 1997-03-06
 NUMBER OF SEQ ID NOS: 63
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 3
 LENGTH: 2332
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-324-867-3

Query Match 93.4%; Score 127; DB 3; Length 2332;
 Best Local Similarity 96.0%; Pred. No. 7.4e-11;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
 Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

Search completed: October 17, 2003, 11:45:06
 Job time : 31 secs

RESULT 14
 US-09-315-179-2
 Sequence 2, Application US/09315179
 Patent No. 6376463
 GENERAL INFORMATION:
 APPLICANT: Lollar, John S
 TITLE OF INVENTION: Modified Factor VIII
 FILE REFERENCE: 75-95H
 CURRENT APPLICATION NUMBER: US/09/315,179
 CURRENT FILING DATE: 1999-05-20
 EARLIER APPLICATION NUMBER: U.S. 09/037,601
 EARLIER FILING DATE: 1998-03-10
 EARLIER APPLICATION NUMBER: 1996-06-26
 EARLIER FILING DATE: 1997-06-26
 EARLIER APPLICATION NUMBER: PCT/US97/11155
 EARLIER FILING DATE: 1997-06-26
 EARLIER APPLICATION NUMBER: PCT/US94/13200

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2003, 11:36:06 ; Search time 69 Seconds
 (Without assignments)
 59,390 Million cell updates/sec

Title: SEQID2-NAT3

Perfect score: 136

Sequence: 1 RPnYSRRLPKGVHLKDFPILPGE: 25

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Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	127	93.4	1438	14	US-10-047-257:-1
3	127	93.4	1438	15	US-10-225-900:-1
4	127	93.4	1471	14	US-10-095-718:-2
5	127	93.4	2332	10	US-09-957-641:-2
6	127	93.4	2332	12	US-10-131-510A:-2
7	127	93.4	2332	15	US-10-187-319:-2
8	127	93.4	2351	15	US-10-132-829:-4
9	127	93.4	2351	15	US-10-172-712:-27
10	101	74.3	1431	14	US-10-095-718:-4
11	94	69.1	2319	12	US-10-131-510A:-6
12	94	69.1	2319	15	US-10-187-319:-6
13	75	55.1	368	12	US-10-131-510A:-4
14	75	55.1	368	15	US-10-187-319:-4
15	75	55.1	1443	12	US-10-131-510A:-39

RESULT 1

US-10-006-091-1

; Sequence 1, Application US/10006091

; Publication No. US20020102730A1

; GENERAL INFORMATION:

; ; APPLICANT: Cho, Myung-Sam

; ; APPLICANT: Chan, Sham-Yuen

; ; APPLICANT: Kelsey, William

; ; APPLICANT: Yee, Helena

; ; TITLE OF INVENTION: Expression System for Factor VIII

; ; FILE REFERENCE: MSB-7255.1

; ; CURRENT APPLICATION NUMBER: US/10/006,091

; ; CURRENT FILING DATE: 2001-12-06

; ; NUMBER OF SEQ ID NOS: 2

; ; SOFTWARE: PatentIn Ver. 2.0

; ; SEQ ID NO 1

; ; LENGTH: 1438

; ; TYPE: PRT

; ; ORGANISM: Artificial Sequence

; ; FEATURE:

; ; OTHER INFORMATION: Description of Artificial Sequence

; ; OTHER INFORMATION: Derived from

; ; US-10-006-091-1

; ; Query Match

; ; Best Local Similarity

; ; Matches

; ; Pred. No. 1.3e-10;

; ;保守型

; ; 0; Mismatches

; ; 1;

; ; Indels

; ; Gaps

; ; 0;

; ; RESULT 2

; ; US-10-047-257-1

; ; Sequence 1, Application US/10047257

; ; Publication No. US20020115152A1

; ; GENERAL INFORMATION:

; ; Sequence 39, Application

; ; Sequence 37, Application

; ; Sequence 37, Application

; ; Sequence 49, Application

; ; Sequence 8, Application

; ; Sequence 11, Application

; ; Sequence 7, Application

; ; Sequence 11, Application

```

; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255.2
; CURRENT APPLICATION NUMBER: US/10/047,257
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO: 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
; OTHER INFORMATION: human factor VIII sequence
US-10-047-257-1

Query Match 93.4%; Score 127; DB 14; Length 1438;
Best Local Similarity 96.0%; Pred. No. 1.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 3
US-10-225-900-1
; Sequence 1, Application US/10225900
; Publication No. US2003007752A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myung-Sam
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelsey, William
; APPLICANT: Yee, Helena
; TITLE OF INVENTION: Expression System for Factor VIII
; FILE REFERENCE: MSB-7255
; CURRENT APPLICATION NUMBER: US/10/225,900
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US/09/209,916
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO: 1
; LENGTH: 1438
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-10-225-900-1

Query Match 93.4%; Score 127; DB 15; Length 1438;
Best Local Similarity 96.0%; Pred. No. 1.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 4
US-10-095-718-2
; Sequence 2, Application US/10095718
; Publication No. US20020131956A1
; GENERAL INFORMATION:
; APPLICANT: Walsh, Christopher
; APPLICANT: Chao, Hengjun
; APPLICANT: Burstein, Haim
; APPLICANT: Lynch, Carmel
; APPLICANT: Stepan, Tony
; APPLICANT: Munson, Keith
; TITLE OF INVENTION: Aden-Associated Virus Vectors Encoding Factor VIII and Methods of Using the Same
; FILE REFERENCE: 35052/204375
; CURRENT APPLICATION NUMBER: US/10/095,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/689,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: Homo sapiens B-domain deleted factor VIII
; FEATURE:
; OTHER INFORMATION: Homo sapiens BDD FVIII
US-10-095-718-2

Query Match 93.4%; Score 127; DB 14; Length 1471;
Best Local Similarity 96.0%; Pred. No. 1.4e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
Db 503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 5
US-09-957-641-2
; Sequence 2, Application US/09957641
; Publication No. US20020182670A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: 75-00
; CURRENT APPLICATION NUMBER: US/09/957,641
; CURRENT FILING DATE: 2001-09-16
; PRIOR APPLICATION NUMBER: US 60/234047
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/236460
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-641-2

Query Match 93.4%; Score 127; DB 10; Length 2332;
Best Local Similarity 96.0%; Pred. No. 2.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 6
US-10-131-510A-2
; Sequence 2, Application US/10131510A
; Publication No. US20030166536A1
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S
; TITLE OF INVENTION: Modified Factor VIII
; FILE REFERENCE: 75-95J
; CURRENT APPLICATION NUMBER: US/10/131,510A
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: U.S. 09/315,179
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: U.S. 09/037,601
; APPLICANT: Walsh, Christopher
; APPLICANT: Chao, Hengjun
; APPLICANT: Burstein, Haim
; APPLICANT: Lynch, Carmel
; APPLICANT: Stepan, Tony
; APPLICANT: Munson, Keith
; TITLE OF INVENTION: Aden-Associated Virus Vectors Encoding Factor VIII and Methods of Using the Same
; FILE REFERENCE: 35052/204375
; CURRENT APPLICATION NUMBER: US/10/095,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/689,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1471
; TYPE: PRT
; ORGANISM: Homo sapiens B-domain deleted factor VIII
; FEATURE:
; OTHER INFORMATION: Homo sapiens BDD FVIII
US-10-131-510A-2

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PRIOR FILING DATE: 1996-03-10
; PRIOR APPLICATION NUMBER: U.S. 08/670,707
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: PCT/US97/11255
; PRIOR FILING DATE: 1997-06-26
; PRIOR APPLICATION NUMBER: PCT/US94/13200
; PRIOR FILING DATE: 1994-11-15
; PRIOR APPLICATION NUMBER: U.S. 08/212,133
; PRIOR FILING DATE: 1994-03-11
; PRIOR APPLICATION NUMBER: U.S. 07/864,004
; PRIOR FILING DATE: 1992-04-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2332
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-131-510A-2

Query Match 95.4%; Score 127; DB 12; Length: 2332;
Best Local Similarity 96.0%; Pred. No. 2.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 7
US-10-187-319-2
; Sequence 2, Application US/10187319
; Publication No. US20030068785A1
; GENERAL INFORMATION:
; APPLICANT: Loilier, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greelee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/187,319
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/523,656
; FILING DATE: 2000-03-10
; APPLICATION NUMBER: US 09/037,601
; FILING DATE: 1998-C3-10
; APPLICATION NUMBER: WO PCT/US97/11155
; FILING DATE: 1997-06-26
; APPLICATION NUMBER: US 08/670,7C7
; FILING DATE: 1996-06-26
; ATTORNEY/AGENT INFORMATION:
; NAME: Greelee, Lorance L.
; REGISTRATION NUMBER: 27,894
; REFERENCE/DOCKET NUMBER: 75-95K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2332 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: <Unknown>
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Liver
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-10-187-319-2

Query Match 93.4%; Score 127; DB 15; Length 2332;
Best Local Similarity 96.0%; Pred. No. 2.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
Db 484 RPLYSRRLPKGVKHLKDFPILPGEI 508

RESULT 8
US-10-132-829-4
; Sequence 4, Application US/10132829
; Publication No. US20030044982A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R.
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor
; FILE REFERENCE: 6627-PA1170
; CURRENT APPLICATION NUMBER: US/10/132,829
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,314
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 5
; SCFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2351
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-132-829-4

Query Match 93.4%; Score 127; DB 15; Length 2351;
Best Local Similarity 96.0%; Pred. No. 2.3e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPNSRRLPKGVKHLKDFPILPGEI 25
Db 503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 9
US-10-172-712-27
; Sequence 27, Application US/10172712
; Publication No. US20030125232A1
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, JOHN H.
; APPLICANT: GALE, ANDREW J.
; APPLICANT: GETZOFF, ELIZABETH D.
; APPLICANT: PELLEQUER, JEAN-LUC
; TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISSULFIDE BONDS
; FILE REFERENCE: 4198-4001US1
; CURRENT APPLICATION NUMBER: US/10/172,712
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 60/298,578
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 2351
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-172-712-27

Query Match 93.4%; Score 127; DB 15; Length 2351;
 Best Local Similarity 96.0%; Pred. No. 2.3e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPNYSRRLPKGVKHLKDFPILPGEI 25
 Db 503 RPLYSRRLPKGVKHLKDFPILPGEI 527

RESULT 10
 US-10-035-718-4
 ; Sequence 4, Application US/10095718
 ; Publication No. US20020131956A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walsh, Christopher
 ; APPLICANT: Chao, Hengjun
 ; APPLICANT: Burstein, Haim
 ; APPLICANT: Lynch, Carmel
 ; APPLICANT: Stepan, Tony
 ; APPLICANT: Munson, Keith
 ; TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
 ; FILE REFERENCE: 35052/204375
 ; CURRENT APPLICATION NUMBER: US/10/095,718
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIORITY APPLICATION NUMBER: 09/689,430
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/158,780
 ; PRIOR FILING DATE: 1999-10-12
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 1431
 ; TYPE: PRT
 ; ORGANISM: Canine B-domain deleted factor VIII
 US-10-095-718-4

Query Match 93.4%; Score 127; DB 15; Length 2351;
 Best Local Similarity 96.0%; Pred. No. 2.3e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PNYSRRLPKGVKHLKDFPILPGEI 25
 Db 498 PLHTGRLPKGVKHLKDFPILPGEI 521

RESULT 11
 US-10-131-510A-6
 ; Sequence 6, Application US/10131510A
 ; Publication No. US20030166536A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S
 ; TITLE OF INVENTION: Modified Factor VIII
 ; FILE REFERENCE: 75-95J
 ; CURRENT APPLICATION NUMBER: US/10/131,510A
 ; PRIOR APPLICATION NUMBER: U.S. 09/315,179
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: U.S. 09/037,601
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: U.S. 08/670,707
 ; PRIOR FILING DATE: 1996-06-26
 ; PRIOR APPLICATION NUMBER: PCT/US97/11155
 ; PRIOR FILING DATE: 1997-06-26
 ; PRIOR APPLICATION NUMBER: PCT/US94/13200
 ; PRIOR FILING DATE: 1994-11-15
 ; PRIOR APPLICATION NUMBER: U.S. 08/212,133
 ; PRIOR FILING DATE: 1994-03-11
 ; PRIOR APPLICATION NUMBER: U.S. 07/864,004
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patentin Ver. 2.0

Query Match 69.1%; Score 94; DB 12; Length 2319;
 Best Local Similarity 66.7%; Pred. No. 2.6e-05;
 Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNYSRRLPKGVKHLKDFPILPGEI 25
 Db 504 PLHARRLPRGIKVHKDLP1HPGEI 527

RESULT 12
 US-10-187-319-6
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S.
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GreenLee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/187,319
 ; FILING DATE: 27-Aug-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/523,656
 ; FILING DATE: 2000-03-10
 ; APPLICATION NUMBER: US 09/037,601
 ; FILING DATE: 1998-03-10
 ; APPLICATION NUMBER: WO PCT/US97/11155
 ; FILING DATE: 1997-06-26
 ; APPLICATION NUMBER: US 08/670,707
 ; FILING DATE: 1996-06-26
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GreenLee, Lorance L.
 ; REGISTRATION NUMBER: 27,894
 ; REFERENCE/DOCKET NUMBER: 75-95K
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 303/499-8080
 ; TELEFAX: 303/499-8089
 ; TITLE: Sequence of the Murine Factor VIII cDNA
 ; JOURNAL: Genomics
 ; VOLUME: 16
 ; PAGES: 374-379
 ; DATE: 1993
 ; RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 2319
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-187-319-6

Query Match 69.1%; Score 94; DB 15; Length 2319;
 Best Local Similarity 66.7%; Pred. No. 2.6e-05;
 Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 PNYSRRLPKGVKHLKDFPILPGEI 25
 Db 504 PLHARRLPRGIKVHKDLP1HPGEI 527

RESULT 13
 US-10-131-510A-4

Sequence 4, Application US/10131510A
 ; Publication No. US20030166536A1
 ; GENERAL INFORMATION: Modified Factor VIII
 ; APPLICANT: Lollar, John S
 ; TITLE OF INVENTION: Modified Factor VIII
 ; FILE REFERENCE: 75-95J
 ; CURRENT APPLICATION NUMBER: US/10/131,510A
 ; CURRENT FILING DATE: 2002-07-10
 ; PRIORITY APPLICATION NUMBER: U.S. 09/315,179
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIORITY APPLICATION NUMBER: U.S. 09/037,691
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIORITY APPLICATION NUMBER: U.S. 08/670,737
 ; PRIOR FILING DATE: 1996-06-26
 ; PRIORITY APPLICATION NUMBER: PCT/US97/11155
 ; PRIOR FILING DATE: 1997-06-26
 ; PRIORITY APPLICATION NUMBER: PCT/US94/13200
 ; PRIOR FILING DATE: 1994-11-15
 ; PRIORITY APPLICATION NUMBER: U.S. 06/212,133
 ; PRIOR FILING DATE: 1994-03-11
 ; PRIORITY APPLICATION NUMBER: U.S. 07/864,604
 ; PRIOR FILING DATE: 1992-04-07
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 368
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 ; JS-10-131-510A-4

Query Match 55.1%; Score 75; DB 15; Length 368;
 Best Local Similarity 83.3%; Pred. No. 0.0027; Matches 15; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLPKGVKHLKDFPILPGE 24
 Db 118 RLKGWVKHLKDMFILPGE 135

RESULT 14
 US-10-187-319-4
 ; Sequence 4, Application US/10187319
 ; Publication No. US20030068785A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S
 ; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circie Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80303

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/187,319
 FILING DATE: 27-Aug-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/523,656
 FILING DATE: 2000-03-10
 APPLICATION NUMBER: US 09/037,601
 FILING DATE: 1998-03-10

APPLICATION NUMBER: WO PCT/US97/11155
 FILING DATE: 1997-06-26
 APPLICATION NUMBER: US 08/670,707
 FILING DATE: 1996-06-26

NAME: Greenlee, Lorance L.
 REGISTRATION NUMBER: 27,894
 REFERENCE/DOCKET NUMBER: 75-95K
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/499-8080
 TELEFAX: 303/499-8089
 INFORMATION FOR SEQ ID NO: 4;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 368 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Porcine
 TISSUE TYPE: spleen
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..368
 OTHER INFORMATION: *note* Predicted amino acid sequence of porcine factor VIII A2 domain, defined as residues homologous to human factor VIII, amino acids 373-740. Residues 1-4 are from known porcine amino acid sequence."
 SEQUENCE DESCRIPTION: SEQ ID NO: 4;
 US-10-187-319-4

Query Match 55.1%; Score 75; DB 15; Length 368;
 Best Local Similarity 83.3%; Pred. No. 0.0027; Matches 15; Mismatches 0; Indels 0; Gaps 0;

QY 7 RLPKGVKHLKDFPILPGE 24
 Db 118 RLKGWVKHLKDMFILPGE 135

RESULT 15
 US-10-131-510A-39
 Sequence 39, Application US/10131510A
 ; Publication No. US20030166536A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lollar, John S
 ; TITLE OF INVENTION: Modified Factor VIII
 ; FILE REFERENCE: 75-95J
 ; CURRENT APPLICATION NUMBER: US/10/131,510A
 ; CURRENT FILING DATE: 2002-07-10
 ; PRIOR APPLICATION NUMBER: U.S. 09/315,179
 ; PRIOR FILING DATE: 1999-05-20
 ; PRIOR APPLICATION NUMBER: U.S. 09/037,601
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: U.S. 08/670,707
 ; PRIOR FILING DATE: 1996-06-26
 ; PRIOR APPLICATION NUMBER: PCT/US97/11155
 ; PRIOR FILING DATE: 1997-06-26
 ; PRIOR APPLICATION NUMBER: PCT/US94/13200
 ; PRIOR FILING DATE: 1994-11-15
 ; PRIOR FILING DATE: 1994-03-11
 ; PRIOR APPLICATION NUMBER: U.S. 08/212,133
 ; PRIOR FILING DATE: 1994-03-11
 ; PRIOR APPLICATION NUMBER: U.S. 07/864,004
 ; PRIOR FILING DATE: 1992-04-07
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 39
 ; LENGTH: 1443
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: factor VIII lacking
 ; OTHER INFORMATION: the B domain
 ; US-10-131-510A-39

ATTORNEY/AGENT INFORMATION:

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Query Match: 55.1%; Score 75; Db 12; Length 1445;
Best Local Similarity 83.38; Pred. No. 0.012;
Matches 15; Conservative 0; Mismatches 3; Indices 2; Caps 0;
Qy      7 RLPKGVKHLKDFPILPGE 24
        ||| |!!! i!!! i!!!
Db      509 RLLKGWVKHLKMPILPGE 526
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Search completed: October 17, 2003, 11:46:54
Job time : 70 secs